

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:45 ; Search time 14.38 seconds
(without alignments)
783.994 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760
Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	99.1	156	2 JE0141	cyclin dependent k
2	529	69.6	130	2 I78845	p15INK4b - mouse
3	522	68.7	138	2 B55479	CDK4 inhibitor p14
4	461.5	60.7	167	2 I58352	p16INK4a - mouse
5	258	33.9	164	2 A57378	cyclin-dependent k
6	249	32.8	166	2 A57379	CDK4/CDK6 inhibito
7	244	32.1	166	2 B57378	cyclin-dependent k
8	231.5	30.5	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	30.1	168	2 A55479	CDK6 inhibitor p18
10	209	27.5	41	2 I52720	gene p15INK4B prot
11	158	20.8	3924	2 S37431	ankyrin 2, neurona
12	137.5	18.1	1848	2 S37771	ankyrin, erythrocy
13	137.5	18.1	1862	2 I49502	ankyrin - mouse
14	133.5	17.6	1836	2 B35049	ankyrin 1, erythro
15	133.5	17.6	1880	2 A35049	ankyrin 1, erythro
16	133.5	17.6	1881	1 SJHUK	ankyrin 1, erythro
17	131	17.2	857	2 S62694	potassium channel
18	130.5	17.2	1423	1 I37275	death-associated p
19	130	17.1	838	2 S23606	potassium channel
20	130	17.1	1765	2 T42714	ankyrin 3, splice
21	130	17.1	1940	2 T42715	ankyrin 3, splice
22	130	17.1	1943	2 T42713	ankyrin 3, splice
23	130	17.1	1961	2 T42716	ankyrin 3, splice
24	128	16.8	4377	2 A55575	ankyrin 3, long sp
25	127.5	16.8	1786	2 A57282	ankyrin-related pr
26	127.5	16.8	1815	2 T15346	elegans ankyrin-re
27	127.5	16.8	1867	2 T15344	ankyrin-related un
28	127.5	16.8	2039	2 T15347	ankyrin-related un
29	126	16.6	247	2 D84448	probable ankyrin [

30	125	16.4	1964	2 T09059	notch4 - mouse
31	124.5	16.4	209	2 T15888	hypothetical prote
32	121	15.9	237	2 T50984	related to 26s pro
33	121	15.9	888	2 D84650	probable potassium
34	120	15.8	476	2 T23213	hypothetical prote
35	118.5	15.6	347	2 C40858	GA-binding protein
36	118.5	15.6	382	2 B40858	GA-binding protein
37	117.5	15.5	347	2 C48146	nuclear respirator
38	117.5	15.5	348	2 I38744	nuclear respirator
39	117.5	15.5	360	2 I38743	nuclear respirator
40	117.5	15.5	395	2 I38741	nuclear respirator
41	117	15.4	1435	2 T32930	hypothetical prote
42	116	15.3	1058	2 T13940	ankyrin - fruit fl
43	115.5	15.2	1058	2 D82654	potassium channel
44	114	15.0	828	2 T52046	transmembrane prot
45	114	15.0	2437	2 S42612	

ALIGNMENTS

RESULT 1

JE0141
N: cyclin dependent kinase inhibitor - human
N: Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor
C: Species: Homo sapiens (man)
C: Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
C: Accession: JE0141; I59268; S39359; I59585; JC5679
R: Huang, C.G.; Deng, W.; Fu, J.L.
C: Chin. J. Biotechnol. 13, 105-107, 1997
A: Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.
A: Reference number: JE0141
A: Accession: JE0141
A: Molecule type: mRNA
A: Residues: 1-156 <HQA>
R: Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994
A: Title: Mutations and altered expression of p16INK4 in human cancer.
A: Reference number: I59268; MUID:95062202
A: Accession: I59268
A: Status: translation not shown; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-152 <OKA>
A: Cross-references: GB:I27211; NID:g558656; PIDN:AAA92554.1; PID:g558657
A: Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925
R: Serrano, M.; Hannon, G.J.; Beach, D. Nature 366, 704-707, 1993
A: Title: A new regulatory motif in cell-cycle control causing specific inhibition of
A: Reference number: S39359; MUID:94081956
A: Accession: S39359
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 9-34, 'V', 'V', '36-156 <SER>
A: Note: this sequence is corrected in reference I59268
R: Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavitigian, S.V.; Science 264, 436-440, 1994
A: Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A: Reference number: I59585; MUID:94204645
A: Accession: I59585
A: Status: translation not shown; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 51-152 <KAM>
A: Cross-references: GB:S69804; NID:g546272; PIDN:AAI4048.1; PID:g4261748
C: Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1
C: Genetics:
A: Gene: GDB:CDKN2A; CDK4I; MLM; PI6; INK4; MTS1; CMM2; CDKN2
A: Cross-references: GDB:335362; OMIM:600160
A: Map position: 9p21-9p21
C: Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
C: Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 99.1%; Score 753; DB 2; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.5e-64;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEVRALLEAVLPNPNAPNSYGRRPQVMMGSGARVAEILLHGA 60
DB 9 MEPSADWLATAAARGVEVRALLEAVLPNPNAPNSYGRRPQVMMGSGARVAEILLHGA 68
QY 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 69 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 128
QY 121 YLRAAAGGTRGSNHRIDAAEGSDIPD 148
DB 129 YLRAAAGGTRGSNHRIDAAEGSDIPD 156

RESULT 2
I78845
p15INK4b - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
C:Accession: I78845
R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W
Oncogene 11, 635-645, 1995
A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.
A:Reference number: I58352; MUID:95380169

A:Accession: I78845
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <RES>
A:Cross-references: GB:S79252; NID:g1087092; PID:g1087093
C:Genetics:
A:Gene: p15INK4b
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology

Query Match 69.6%; Score 529; DB 2; Length 130;
Best Local Similarity 88.3%; Pred. No. 2.5e-43;
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAAARGVEVRALLEAVLPNPNAPNSYGRRPQVMMGSGARVAEILLHGAEPNCADP 67
DB 10 LATAAARGVETVRQLLEAGADPNALNRFGRRPQVMMGSAQVAEILLHGAEPNCADP 69
QY 68 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARAAAG 127
DB 70 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDIARYLHAATG 129

RESULT 3
B55479
CDK4 inhibitor p14(INK4B/MTS2) - human
N:Alternate names: CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000
C:Accession: B55479; S47593; I81183; I52713
R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;
Genes Dev. 8, 2939-2952, 1994
A:Title: Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6
A:Reference number: A55479; MUID:95095079
A:Accession: B55479
A:Molecule type: mRNA
A:Residues: 1-138 <GUA>

A:Cross-references: GB:U17075; NID:g639715; PIDN:AAC50075.1; PID:g639716
A:Experimental source: HeLa cells
R:Hannon, G.J.; Beach, D.
Nature 371, 257-261, 1994
A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.
A:Reference number: S47593; MUID:94359613
A:Accession: S47593
A:Molecule type: mRNA
A:Residues: 1-19, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>

A:Cross-references: GB:I36844; NID:g556197; PIDN:AAA50282.1; PID:g556198
A:Experimental source: HaCat cells
R:kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;
Science 264, 436-440, 1994
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A:Reference number: I59585; MUID:94204645

A:Accession: I81183
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 53-138 <KAM>
A:Cross-references: GB:S69805; NID:g546273; PIDN:AAD14049.1; PID:g4261749
R:Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.;
Cancer Res. 54, 6353-6358, 1994
A:Title: Deletion of p16 and p15 genes in brain tumors.
A:Reference number: I52713; MUID:95079408

A:Accession: I52713
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-52 <RES>
A:Cross-references: GB:S75756; NID:g861470; PIDN:AAD14186.1; PID:g4261886
C:Genetics:
A:Gene: GDB:CDKN2B; MTS2
A:Cross-references: GDB:579577; OMIM:600431
A:Map position: 9p21-9p21
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homol
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 68.7%; Score 522; DB 2; Length 138;
Best Local Similarity 85.5%; Pred. No. 1.2e-42;
Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 SADWLATAAARGVEVRALLEAVLPNPNAPNSYGRRPQVMMGSGARVAEILLHGAEPN 63
DB 14 SDEGLASAAAAGLVKVKVQLLEAGADPNVGRFRRAIQVMMGSAKVAEILLHGAEPN 73
QY 64 CADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVLR 123
DB 74 CADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVLR 133
QY 124 AAAG 127
DB 134 YATG 137

RESULT 4
I58352
p16INK4a - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C:Accession: I58352
R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.
Oncogene 11, 635-645, 1995
A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.
A:Reference number: I58352; MUID:95380169

A:Accession: I58352
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-167 <RES>
A:Cross-references: GB:S79251; NID:g1087090; PID:g1087091
C:Genetics:
A:Gene: p16INK4a
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homol

Query Match 60.7%; Score 461.5; DB 2; Length 167;
Best Local Similarity 63.2%; Pred. No. 8.5e-37;
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

QY 1 MEPSADWLATAAARGVEVRALLEAVLPNPNAPNSYGRRPQVMMGSGARVAEILLHGA 60
DB 1 MESAADRLA-RAAQGRVHDVRLLEAGVSPNAPNSGRTPTIQVMMGNVHVAALLNNGA 59

RESULT 7

best local similarity 45.7%; Fied. NO. 48-10;
Matches 69; Conservative 18; Mismatches 53; Indels 18; Gaps 5;

DO 123 ESDJHHRGSHLIF EELERKQGRQNH FDLUQGHNNLF 103

best local similarity 40.3%, Fred. NO. 0.2e-19;
Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;

DB 3 EPWGNELASAAAGDDELSLTLLQNNVNNAQNGFRTALQVMKLGNPETARLLUURGN 62

QV 62 PNCADPATLTPRVHDAAREGEFLDTLLVVLHAGARGLDVRDAGWGLRPVDLAEEELGHRDVARY 1121

Db 63 PNLKD-GTGFVHDAARAGFLDTVQALLFEQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121

QY 122 LRAAAGGTRGSNHARIDAA 140

Db 122 LMKHTACNVGHRNHKGDTA 140

RESULT 9

A55479

CDK6 inhibitor p18 - human

N:Alternate names: cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase

C:Species: Homo sapiens (man)

C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Sep-1999

C:Accession: A55479

R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;

Genes Dev. 8, 2939-2952, 1994

A:Title: Growth suppression by p18, a p16(INK4B/MTS2)-related CDK6 i

A:Reference number: A55479; MUID:95095079

A:Accession: A55479

A:Molecule type: mRNA

A:Residues: 1-168 <GUA>

A:Cross-references: GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714

C:Genetics:

A:Gene: GDB:CDKN2C

A:Cross-references: GDB:594931

A:Map position: lp32-lp32

C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology

C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 30.1%; Score 228.5; DB 2; Length 168;

Best Local Similarity 40.3%; Pred. No. 1.2e-14;

Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;

QY 2 EPSADWLATAAARGVEEVRALAEVALPNAPNSYGRPRIQVMGMSARVAELLHLHGAE 61

Db 3 EPNGNELASAAAGDLEQLTSLNQNVAQNGFRTALQVMKLGNPETARRLLRGAN 62

QY 62 PNCADPATLTPRVHDAAREGFLDTVLVLRHAGARLDVRANGRLPVDLAEELGHRDVARV 121

Db 63 POLKD-RTGFVHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEF 121

QY 122 LRAAAGGTRGSNHARIDAA 140

Db 122 LVKHTASNVGHRNHKGDTA 140

RESULT 10

I52720

gene p15INK4B protein - rat (fragment)

C:Species: Rattus sp. (rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000

C:Accession: I52720

R:Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.

Cancer Res. 55, 1607-1612, 1995

A:Title: Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithel

A:Reference number: I52720; MUID:95228036

A:Accession: I52720

A:Molecule type: DNA

A:Residues: 1-41 <RES>

A:Cross-references: GB:S77734; NID:g998711

C:Genetics:

A:Gene: p15INK4B

C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology

Query Match 27.5%; Score 209; DB 2; Length 41;

Best Local Similarity 97.6%; Pred. No. 1.7e-13;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAQVAELLHLHGAPNCADPATLTPRVHDAAREGFLD 84

Db 1 MMGSAQVAELLHLHGAPNCADPATLTPRVHDAAREGFLD 41

RESULT 11

S37431

ankryrin 2, neuronal long splice form - human

N:Alternate names: ankryrin B, 440K splice form; ankryrin-B; brain ankryrin; non-erythro

N:Contains: ankryrin 2, short form

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999

C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569

R:Chan, W.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37431

A:Accession: S37431

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-3924 <CHA>

A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288

R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 114, 241-253, 1991

A:Title: Isolation and characterization of cDNAs encoding human brain ankryrins reveal

A:Reference number: A39643; MUID:91302466

A:Accession: A39643

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2077 <OT1>

A:Cross-references: GB:X56957

A:Accession: B39643

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1443,3585-3924 <OTT>

A:Cross-references: EMBL:X56958

R:Ts'e, W.T.; Wenninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa

Genomics 10, 858-866, 1991

A:Title: Isolation and chromosomal localization of a novel nonerythroid ankryrin gene.

A:Reference number: A40334; MUID:92009921

A:Accession: A40334

A:Molecule type: DNA

A:Residues: 463-474, 'PE', 477-495 <TSE>

A:Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648

R:Chan, W.; Kordeli, E.; Bennett, V.

J. Cell Biol. 123, 1463-1473, 1993

A:Title: 440-kD ankryrinB: structure of the major developmentally regulated domain and

A:Reference number: A49462; MUID:94075409

A:Accession: A49462

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-3924 <RES>

A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288

C:Genetics:

A:Gene: GDB:ANK2

A:Cross-references: GDB:127607; OMIM:106410

A:Map position: 4q25-4q27

C:Superfamily: ankryrin; ankryrin repeat homology

C:Keywords: alternative splicing

F:2-3924/Product: ankryrin 2, long form #status predicted <MAT>

F:2-1443,3585-3924/Product: ankryrin 2, short form #status predicted <MA2>

F:63-95/Domain: ankryrin repeat homology <AN01>

F:96-128/Domain: ankryrin repeat homology <AN02>

F:129-161/Domain: ankryrin repeat homology <AN03>

F:162-190/Domain: ankryrin repeat homology <AN04>

F:191-223/Domain: ankryrin repeat homology <AN05>

F:232-264/Domain: ankryrin repeat homology <AN06>

F:265-297/Domain: ankryrin repeat homology <AN07>

F:298-330/Domain: ankryrin repeat homology <AN08>

F:331-363/Domain: ankryrin repeat homology <AN09>

F:364-396/Domain: ankryrin repeat homology <AN10>

F:397-429/Domain: ankryrin repeat homology <AN11>

F:430-462/Domain: ankryrin repeat homology <AN12>

F:463-495/Domain: ankryrin repeat homology <AN13>

F:496-528/Domain: ankryrin repeat homology <AN14>

F:529-561/Domain: ankryrin repeat homology <AN15>

Query Match 18.1%; Score 137.5; DB 2; Length 1848;
Best Local Similarity 34.7%; Pred. No. 8e-05;
Matches 51; Conservative 17; Mismatches 68; Indels 11; Gaps 6;

[illegible]

C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
C:Accession: A35049
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370
A:Accession: A35049
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1880 <LAM>
A:Cross-references: GB:M28880
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; cytoskeleton
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>

RESULT 14
B35049
ankyrin 1, erythrocyte splice form 3 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
C:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C:Accession: B35049
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370
A:Accession: B35049
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1856 <LAM>
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 17.6%; Score 133.5; DB 2; Length 1880;
Best Local Similarity 35.4%; Pred. No. 0.0002;
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;
QY 8 LATAAARGVEVRALLEAVLPNAPNSYGRPTQV-MMMSARVAELLLHGAEPNCAD 66
Db 507 LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 566
QY 67 PATLTPRVHDAAREGFLDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL-- 122
Db 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAANGYTPPLHTAAKQNOVEVARSLIQ 623
QY 123 ---RAAGGTRGSNHARIDAAGPSDI 146
Db 624 YGGSANAESVQGVTPPLHLAAQEGHAEM 650

Query Match 17.6%; Score 133.5; DB 2; Length 1856;
Best Local Similarity 35.4%; Pred. No. 0.00019;
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;
QY 8 LATAAARGVEVRALLEAVLPNAPNSYGRPTQV-MMMSARVAELLLHGAEPNCAD 66
Db 507 LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 566
QY 67 PATLTPRVHDAAREGFLDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL-- 122
Db 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAANGYTPPLHTAAKQNOVEVARSLIQ 623
QY 123 ---RAAGGTRGSNHARIDAAGPSDI 146
Db 624 YGGSANAESVQGVTPPLHLAAQEGHAEM 650

Search completed: May 7, 2002, 12:33:45
Job time: 120 sec

RESULT 15
A35049
ankyrin 1, erythrocyte splice form 2 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
C:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:33:25 ; Search time 11.7 seconds
(without alignments)
463.794 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760
Sequence: 1 MEPSADWLATAAARGRVEEY.....TRGSNHARIDAAEGPSDIPD 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	753	99.1	156	1	CDN2_HUMAN
2	529	69.6	130	1	CDN5_MOUSE
3	524	68.9	130	1	CDN5_RAT
4	522	68.7	138	1	CDN5_HUMAN
5	461.5	60.7	167	1	CDN2_MOUSE
6	408	53.7	171	1	CDN2_MONDO
7	259	34.1	166	1	CDN7_HUMAN
8	249	32.8	166	1	CDN7_MOUSE
9	231.5	30.5	168	1	CDN6_MOUSE
10	228.5	30.1	168	1	CDN6_HUMAN
11	158	20.8	3924	1	ANK2_HUMAN
12	137.5	18.1	1862	1	ANK1_MOUSE
13	133.5	17.6	768	1	YB23_HUMAN
14	133.5	17.6	1880	1	ANK1_HUMAN
15	130.5	17.2	1431	1	DAFK_HUMAN
16	125	16.4	1359	1	NTC4_MOUSE
17	123	16.2	1059	1	Y379_HUMAN
18	118.5	15.6	347	1	GABC_MOUSE
19	118.5	15.6	382	1	GABB_MOUSE
20	117.5	15.5	347	1	GABC_HUMAN
21	117.5	15.5	383	1	GABB_HUMAN
22	114	15.0	768	1	BARL_RAT
23	114	15.0	2437	1	NOTC_BRARE
24	111.5	14.7	2531	1	NTCL_RAT
25	111	14.6	323	1	ANKH_CHRVI
26	111	14.6	777	1	BARL_HUMAN
27	110.5	14.5	2444	1	NTCL_HUMAN
28	109.5	14.4	832	1	ANK3_HUMAN
29	107.5	14.1	2703	1	NOTC_DROME
30	107	14.1	765	1	BARL_MOUSE
31	104.5	13.8	2524	1	NOTC_XENLA
32	103.5	13.6	2318	1	NTC3_MOUSE
33	102.5	13.5	740	1	Y050_HUMAN

RESULT 1

ID	CDN2_HUMAN	STANDARD	PRT	156 AA.
AC	P42771; Q15191;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	15-JUL-1998 (Rel. 40, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4A)			
DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).			
GN	CDKN2A OR CDKN2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94081956; PubMed=8259215;			
RA	Serrano M., Hannon G.J., Beach D.;			
RA	"A new regulatory motif in cell-cycle control causing specific			
RT	inhibition of cyclin D/CDK4.";			
RL	Nature 366:704-707(1993).			
RN	[2]			
RP	SEQUENCE OF 51-152 FROM N.A.			
RX	MEDLINE=94204645; PubMed=8153634;			
RA	Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,			
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,			
RA	Skolnick M.H.;			
RT	"A cell cycle regulator potentially involved in genesis of many tumor			
RT	types.";			
RL	Science 264:436-440(1994).			
RN	[3]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RX	MEDLINE=96182088; PubMed=8622687;			
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;			
RT	"Regulation of p16CDKN2 expression and its implications for cell			
RT	immortalization and senescence.";			
RL	Mol. Cell. Biol. 16:859-867(1996).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.			
RX	MEDLINE=98421670; PubMed=9751050;			
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;			
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6			
RT	by the tumour suppressor p16INK4a.";			
RL	Nature 395:237-243(1998).			
RN	[5]			
RP	REVIEW ON MELANOMA VARIANTS.			
RX	MEDLINE=96377761; PubMed=8783570;			
RA	Dracopoli N.C., Fountain J.W.;			
RT	"CDKN2 mutations in melanoma.";			
RL	Cancer Surv. 26:115-132(1996).			
RN	[6]			
RP	REVIEW ON VARIANTS.			
RX	MEDLINE=96303699; PubMed=8723678;			
RA	Smith-Soerensen B., Hovig E.;			
RT	"CDKN2A (p16INK4A) somatic and germline mutations.";			
RL	Hum. Mutat. 7:294-303(1996).			

34	100.5	13.2	414	1	GABD_MOUSE	P81069 mus musculus
35	100.5	13.2	500	1	CACT_DROME	Q03017 drosophila
36	100.5	13.2	1178	1	PH81_YEAST	P17442 saccharomyc
37	99.5	13.1	1454	1	KDGE_DROME	Q09103 drosophila
38	96.5	12.7	571	1	GLS1_CAEEL	Q09103 caenorhabdi
39	96	12.6	679	1	RNSA_MOUSE	Q05921 mus musculus
40	93.5	12.3	227	1	PHLB_SERLI	P18954 serrattia li
41	93	12.2	471	1	Y148_HUMAN	Q14161 homo sapien
42	91.5	12.0	2531	1	NTC1_MOUSE	Q01705 mus musculus
43	89	11.7	677	1	SKD3_MOUSE	Q60649 mus musculus
44	89	11.7	757	1	HT16_HYDAT	P53356 hydra atten
45	87	11.4	632	1	Y041_HUMAN	Q15057 homo sapien

ALIGNMENTS

[7] VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
RP MEDLINE=9438359; PubMed=8060323;
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
cell lung carcinomas.";
RT cell lung carcinomas.";
RP Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
[8]
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.
RP MEDLINE=95078916; PubMed=7987387;
RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
RT "Germline p16 mutations in familial melanoma.";
RP Nat. Genet. 8:15-21(1994).
[9]
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
RP MEDLINE=95060835; PubMed=7970734;
RA Zhou X., Tarmir L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
RA Abraham J.M., Meltzer S.J.;
RT "The MTS1 gene is frequently mutated in primary human esophageal
tumors.";
RP Oncogene 9:3737-3741(1994).
[10]
RP VARIANTS.
RP MEDLINE=95188190; PubMed=7882351;
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zarwala M.,
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
primary and metastatic lung cancer.";
RP Cancer Res. 55:1448-1451(1995).
[11]
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
RP MEDLINE=96121580; PubMed=8959405;
RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
kindreds.";
RP Hum. Mol. Genet. 4:1845-1852(1995).
[12]
RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
RP MEDLINE=95375774; PubMed=7647780;
RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
RA Dracopoli N.C.;
RT "Mutations associated with familial melanoma impair p16INK4
function.";
RP Nat. Genet. 10:114-116(1995).
[13]
RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
RP MEDLINE=96323259; PubMed=8710906;
RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
RA Iselbacher K.J., Sober A.J., Haber D.A.;
RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in
familial melanoma: analysis of a clinic-based population.";
RP Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
[14]
RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
RP MEDLINE=97472457; PubMed=9328469;
RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,
RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
RA Bishop D.T., Bishop J.N.;
RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
RP Hum. Mol. Genet. 6:2061-2067(1997).
[15]
RP VARIANTS FAMILIAL MELANOMA.
RP MEDLINE=98087572; PubMed=9425228;
RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bomblard J.,
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone
families in France.";
RP Hum. Mol. Genet. 7:209-216(1998).
[16]
RP ERRATUM.
RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bomblard J.,
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
RP Hum. Mol. Genet. 7:941-941(1998).
[17]
RP VARIANT PANCREATIC CARCINOMA CYS-146.
RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,
RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple
pancreatic carcinomas.";
RP Hum. Mutat. 12:70-70(1998).
[18]
RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
RA Gretsardottir S., Olafsdottir G.H., Borg A.;
RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,
glioma and carcinoma of the pancreas.";
RP Hum. Mutat. 12:212-212(1998).
CC -|- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
CC -|- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
CC -|- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
CC WIDE RANGE OF TISSUES.
CC -|- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -|- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L27211; AAA92554.1; -;
DR EMBL; U12820; AAB60645.1; -;
DR EMBL; U12818; AAB60645.1; JOINED.
DR EMBL; U12819; AAB60645.1; JOINED.
DR EMBL; S69804; AAD14048.1; -;
DR EMBL; X94154; CAA63870.1; -;
DR PDB; 1BI7; 16-FEB-99.
DR MIM; 600160; -;
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.
FT REPEAT 11 40 ANK 1.
FT REPEAT 44 72 ANK 2.
FT REPEAT 77 106 ANK 3.
FT REPEAT 110 139 ANK 4.
FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).
FT FTID=VAR_001408.
FT L -> P (IN A BILIARY TRACT TUMOR AND A
FT FAMILIAL MELANOMA).
FT FTID=VAR_001409.
FT A -> P (IN A LONG TUMOR AND MELANOMA).
FT FTID=VAR_001410.
FT A -> S (IN A BILIARY TRACT TUMOR).
FT FTID=VAR_001411.
FT G -> D (IN A PANCREAS TUMOR).
FT FTID=VAR_001412.
FT R -> C (IN MELANOMA).
FT FTID=VAR_001413.
FT R -> P (IN FAMILIAL MELANOMA AND
FT MELANOMA).
FT FTID=VAR_001414.
FT E -> D (IN A BILIARY TRACT TUMOR).
FT FTID=VAR_001415.

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 3.8e-66;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPRIOVMGMSARVAELLLHGA 60
|||||
Db 9 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPRIOVMGMSARVAELLLHGA 68

QY 61 EPCACDPTATLTPVHDAAREGFLDTLVLLHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
|||||
Db 69 EPCACDPTATLTPVHDAAREGFLDTLVLLHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAAGPSDIPD 148
|||||
Db 129 YLRAAAGTGRGSHARIDAAGPSDIPD 156

RESULT 2
CDN5_MOUSE STANDARD; PRT; 130 AA.
AC P55271;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RA "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:635-645(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J X DBA;
RA MEDLINE=97322242; PubMed=9178896;
RA Malumbres M., de Castro I., Santos J., Melendez B., Manges R.,
Serrano M., Pellicer A., Fernandez-Piqueras J.;
RA "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RL Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U66085; AAB39833.1; -.
CC EMBL; U66084; AAB39833.1; JOINED.
CC MGD; MGI:104737; Cdkn2b.
CC InterPro; IPR002110; ANK.
CC Pfam; PF00023; ank; 3.
CC SMART; SM00248; ANK; 1.
CC PROSITE; PS50088; ANK_REPEAT; 1.

DR PROSITE; PS50297; ANK_REPEAT; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 69.6%; Score 529; DB 1; Length 130;
Best Local Similarity 88.3%; Pred. No. 1.5e-44;
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAAARGVEEVRLLEAVALPNAPNSYGRPRIOVMGMSARVAELLLHGAEPNCADP 67
|||||
Db 10 LATAAARGVETVRLLEAGADPNALNFRGRRPQVMMGSAQVAELLLHGAEPNCADP 69

QY 68 ATLTPVHDAAREGFLDTLVLLHAGARLDVDRDAGRLPVDLAEEELGHRDVARVYLRRAAG 127
|||||
Db 70 ATLTPVHDAAREGFLDTLVLLHAGARLDVDRDAGRLPVDLAEEELGHRDVARVYLRRAAG 129

RESULT 3
CDN5_RAT STANDARD; PRT; 130 AA.
AC P55272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B OR INK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96001392; PubMed=7546221;
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
Tsuchiya H., Kikuchi Y., Mitani H.;
RA "Molecular genetic basis of renal carcinogenesis in the Eker rat
RT model of tuberous sclerosis (Tsc2).";
RL Mol. Carcinog. 14:23-27(1995).
RN [2]
RP SEQUENCE OF 46-86 FROM N.A.
RX MEDLINE=95228036; PubMed=7712460;
RA Knaep D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RA "Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in
FT kidney epithelial cell lines but not primary renal tumors.";
RL Cancer Res. 55:1607-1612(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S79760; AAB35360.1; -.
CC EMBL; S77734; -; NOT_ANNOTATED_CDS.
CC DR

```
DR InterPro: IPR002110; ANK.
DR SMART: PF00023; ank; 3.
DR Pfam: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT CHAIN 46 130 LONG ISOFORM.
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT INIT_MET 46 46 SHORT ISOFORM.
FT REPEAT 5 34 FOR SHORT ISOFORM.
FT REPEAT 38 66 ANK 1.
FT REPEAT 71 100 ANK 2.
FT REPEAT 104 130 ANK 3.
FT REPEAT 130 130 ANK 4.
SQ SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match 68.9%; Score 524; DB 1; Length 130;
Best Local Similarity 86.7%; Pred. No. 4.5e-44;
Matches 104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAAARGVEVRALLEVALPNAPNSYGRPRIOVMGMSARVAEELLLHGAEPNCADP 67
DB 10 LATAAARGVEVRALLEVALPNAPNSYGRPRIOVMGMSARVAEELLLHGAEPNCADP 69
QY 68 ATLTRPVHDAAREGFLDTLVHLHAGARLDVDRDAGRLPVDLAEEELGHRDVARYLRAAAG 127
DB 70 ATLTRPVHDAAREGFLDTLVHLHAGARLDVDRDAGRLPVDLAEEELGHRDVARYLRAAAG 129
RESULT 4
ID CON5_HUMAN STANDARD; PRT; 138 AA.
AC P42772;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DE 20-AUG-2001 (Rel. 40; Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
GN CDKN2B OR MTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95095079; PubMed=8001816;
RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
RA Matera G.A., Xiong Y.;
RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
RT cdK6 inhibitor, correlates with wild-type pRb function.";
RL Genes Dev. 8:2939-2952(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94359613; PubMed=8078588;
RA Hannon G.J., Beach D.;
RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle
RT arrest.";
RL Nature 371:257-261(1994).
RN [3]
RP SEQUENCE OF 53-138 FROM N.A.
RX MEDLINE=94204645; PubMed=8153634;
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [4]
RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
RX MEDLINE=95188190; PubMed=7862351;
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
```

```
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: U17075; AAC50075.1; -.
CC EMBL: L36844; AAA50282.1; -.
CC EMBL: S69805; AAD14049.1; -.
CC MIM: 600431; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; FALSE_NEG.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.
FT REPEAT 13 39 ANK 1 (INCOMPLETE).
FT REPEAT 73 103 ANK 2.
FT VARIANT 47 47 G -> E (IN LUNG ADENOCARCINOMA).
FT VARIANT 50 50 /FTID=VAR_001488.
FT VARIANT 20 21 A -> V (IN LUNG ADENOCARCINOMA).
FT CONFLICT 20 21 /FTID=VAR_001489.
FT CONFLICT 23 23 SA -> TP (IN REF. 2).
FT CONFLICT 32 34 MISSING (IN REF. 2).
FT CONFLICT 32 34 QLL -> HSW (IN REF. 2).
SQ SEQUENCE 138 AA; 14722 MW; 0D6FFBDF6A6FEAD21 CRC64;

Query Match 68.7%; Score 522; DB 1; Length 138;
Best Local Similarity 85.5%; Pred. No. 7.6e-44;
Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 SADWLATAAARGVEVRALLEVALPNAPNSYGRPRIOVMGMSARVAEELLLHGAEPN 63
DB 14 SDEGLASAAARGVEVRALLEVALPNAPNSYGRPRIOVMGMSARVAEELLLHGAEPN 73
QY 64 CADPATLTRPVHDAAREGFLDTLVHLHAGARLDVDRDAGRLPVDLAEEELGHRDVARYLR 123
DB 74 CADPATLTRPVHDAAREGFLDTLVHLHAGARLDVDRDAGRLPVDLAEEELGHRDVARYLR 133
QY 124 AAAG 127
DB 134 TATG 137

RESULT 5
ID CDN2_MOUSE STANDARD; PRT; 167 AA.
AC P51480;
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 20-AUG-2001 (Rel. 40; Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4A).
GN CDKN2A OR P16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```



```
DR MGD; MGI:105387; Cdkn2d.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PSS0088; ANK_REPEAT; 1.  
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.  
FT REPEAT 73 102 ANK 1.  
FT REPEAT 106 135 ANK 2.  
FT REPEAT 138 166 ANK 3.  
FT REPEAT 17 17 A->P (IN REF. 2).  
FT CONFLICT 17 17  
SQ SEQUENCE 166 AA; 17894 MW; 9E74F5C23B7EBCB2 CRC64;  
  
Query Match 32.8%; Score 249; DB 1; Length 166;  
Best Local Similarity 44.3%; Pred. No. 2.5e-17;  
Matches 70; Conservative 18; Mismatches 52; Indels 18; Gaps 5;  
  
QY 6 DLWATAAARGVEVRALL-EAVALPNAPNSYGRPIQVMMGSAARVAELLHGAEPNC 64  
DB 10 DRLSGARAGDVQVRRLHRELVHPDALNRFGKTALQVMFMFGSPAVALLELLKQGASPNV 69  
QY 65 ADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVARYL-- 122  
DB 70 QD-ASGTPVHDAARTGFLDTLVVLRHAGADVNALDSTGSLPIHLAIREGHSVVVSFLAP 128  
QY 123 -----RAAGGT-----RGSNHARIDAEGPSDIP 147  
DB 129 ESDLHRDASGLTPLELARQGAQNL-MDILQGHMMIP 165  
  
RESULT 9  
CDN6_MOUSE STANDARD; PRT; 168 AA.  
AC Q60772;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT  
DE KINASE 4 INHIBITOR C) (P18-INK4C).  
GN CDKN2C.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL KAPLAN;  
RX MEDLINE=95257948; PubMed=7739547;  
RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;  
RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the  
RT cyclin D-dependent kinases CDK4 and CDK6."  
RL Mol. Cell. Biol. 15:2672-2681(1995).  
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS  
CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON  
CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.  
CC -!- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; U19596; AAC52193.1; -  
DR MGD; MGI:105388; Cdkn2c.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
  
DR SMART; SM00248; ANK; 2.  
DR PROSITE; PSS0088; ANK_REPEAT; 2.  
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.  
KW Cell cycle; Repeat; ANK repeat.  
FT REPEAT 4 33 ANK 1.  
FT REPEAT 37 65 ANK 2.  
FT REPEAT 69 98 ANK 3.  
FT REPEAT 102 132 ANK 4.  
FT REPEAT 136 165 ANK 5.  
SQ SEQUENCE 168 AA; 18066 MW; BC88D5489307E128 CRC64;  
  
Query Match 30.5%; Score 231.5; DB 1; Length 168;  
Best Local Similarity 40.3%; Pred. No. 1.3e-15;  
Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;  
  
QY 2 EPSADWLATAAARGVEVRALLEAVALPNAPNSYGRPIQVMMGSAARVAELLHGAE 61  
DB 3 EPWGNELASAAAGDLEQLTSLNNVNNVNAQNGFORTALQVMKGNPFIARRLLRGAN 62  
QY 62 PNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 121  
DB 63 PNLKD-GTGEAVTHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121  
QY 122 LRAAAGTGRGSHARIDAA 140  
DB 122 LMKHTACNVGHRNHKGDTA 140  
  
RESULT 10  
CDN6_HUMAN STANDARD; PRT; 168 AA.  
AC P42773;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT  
DE KINASE 4 INHIBITOR C) (P18-INK4C).  
GN CDKN2C OR CDKN6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95095079; PubMed=8001816;  
RA Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,  
RA Matera G.A., Xiong Y.;  
RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related  
RT CDK6 inhibitor, correlates with wild-type pRB function."  
RL Genes Dev. 8:2939-2952(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.  
RC TISSUE=Breast;  
RX MEDLINE=98300299; PubMed=9636670;  
RA Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;  
RT "Structure of the gene encoding the human cyclin-dependent kinase  
RT inhibitor p18 and mutational analysis in breast cancer."  
RL Biochem. Biophys. Res. Commun. 247:146-153(1998).  
RN [3]  
RP VARIANT BREAST CANCER PRO-72.  
RX MEDLINE=96438606; PubMed=8840966;  
RA Lapointe J., Lachance Y., Labrie Y., Labrie C.;  
RT "A p18 mutant defective in CDK6 binding in human breast cancer  
RT cells."  
RL Cancer Res. 56:4586-4589(1996).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).  
RX MEDLINE=98100086; PubMed=9437433;  
RA Venkataramani R., Swaminathan K., Marmorstein R.;  
RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides  
RT insights into ankyrin-like repeat structure/function and  
RT tumor-derived p16INK4 mutations.";
```



```

FT REPEAT 40 69 ANK 1.
FT REPEAT 73 102 ANK 2.
FT REPEAT 106 135 ANK 3.
FT REPEAT 139 168 ANK 4.
FT REPEAT 170 197 ANK 5.
FT REPEAT 201 230 ANK 6.
FT REPEAT 234 263 ANK 7.
FT REPEAT 267 296 ANK 8.
FT REPEAT 300 329 ANK 9.
FT REPEAT 333 362 ANK 10.
FT REPEAT 366 395 ANK 11.
FT REPEAT 399 428 ANK 12.
FT REPEAT 432 461 ANK 13.
FT REPEAT 465 494 ANK 14.
FT REPEAT 498 527 ANK 15.
FT REPEAT 531 560 ANK 16.
FT REPEAT 564 593 ANK 17.
FT REPEAT 597 626 ANK 18.
FT REPEAT 630 659 ANK 19.
FT REPEAT 663 692 ANK 20.
FT REPEAT 696 725 ANK 21.
FT REPEAT 729 758 ANK 22.
FT REPEAT 762 791 ANK 23.
FT DOMAIN 1399 1483 DEATH.
SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001E5 CRC64;

Query Match 18.1%; Score 137.5; DB 1; Length 1862;
Best Local Similarity 34.7%; Pred. No. 2.4e-05;
Matches 51; Conservative 17; Mismatches 68; Indels 11; Gaps 6;

Qy 8 LATAAARGVEEVRLLEAVALPNAPNSYGRRPQV-MMGSGARVAELLLHGAEPNCAD 66
Db 503 LHTAAREGHVDTALALLEKEASQACMKGFTPLHVAAYGKVRLEALLLEHDAHPNAG 562
Qy 67 PATLTRPVHDAAREGFLDTL-VYLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 122
Db 563 KNGLT-PLHAVHNNLDIVKLLPRGGS--PHSPAWNGYTPHLHIAKQNIQIEVARSLIQ 619
Qy 123 ---RAAAGTGRGSHARIDAAEGPSDI 146
Db 620 YGGSANAESVQGVTPHLHAAQEGHTEM 646

RESULT 13
YB23_HUMAN
ID YB23_HUMAN STANDARD; PRT; 768 AA.
AC Q9ULJ7;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN KIAA1223 (FRAGMENT).
GN KIAA1223.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
CC -!- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB033049; BAA86537.1; -.
CC HSP; P42771; IBI7.
CC InterPro; IPR002110; ANK.
CC Pfam; PF00023; ank; 13.
CC SMART; SM00248; ANK; 13.
CC PROSITE; PS00088; ANK_REPEAT; 13.
CC PROSITE; PS00297; ANK_REPEAT_REGION; 1.
CC KW Hypothetical protein; Repeat; ANK repeat.
FT NON_TER 1 1
FT REPEAT 1 11 ANK 1.
FT REPEAT 15 44 ANK 2.
FT REPEAT 48 82 ANK 3.
FT REPEAT 86 115 ANK 4.
FT REPEAT 119 148 ANK 5.
FT REPEAT 152 181 ANK 6.
FT REPEAT 185 214 ANK 7.
FT REPEAT 218 247 ANK 8.
FT REPEAT 251 280 ANK 9.
FT REPEAT 284 313 ANK 10.
FT REPEAT 317 346 ANK 11.
FT REPEAT 350 379 ANK 12.
FT REPEAT 383 412 ANK 13.
FT REPEAT 416 446 ANK 14.
SQ SEQUENCE 768 AA; 82819 MW; 2913B69BE2DFE06D CRC64;

Query Match 17.6%; Score 133.5; DB 1; Length 768;
Best Local Similarity 33.8%; Pred. No. 2.2e-05;
Matches 49; Conservative 14; Mismatches 75; Indels 7; Gaps 3;

Qy 8 LATAAARGVEEVRLLEAVALPNAPNSYGRRPQV-MMGSGARVAELLLHGAEPNCAD 66
Db 124 LLAASMGHASVNTLLFWGAAVDSIDSEGRVLSIASAQGNVEVRTLDRGLDENHRD 183
Qy 67 PATLTRPVHDAAREGFLDTL-VYLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 122
Db 184 DAGWT-PLHMAAFEGHRLICEALIEQGARTNEIDNDGRIPFILASQEGHYDCVQILLENK 242
Qy 123 -RAAAGTGRGSHARIDAAEGPSDI 146
Db 243 SNIDQGYDGRNALRVAALGHRDI 267

RESULT 14
ANK1_HUMAN
ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
AC P16157;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).
GN ANK1 OR ANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
RC TISSUE=Hematopoietic;
RX MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.";
RL Nature 344:36-42(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175370; PubMed=1689849;
RA Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
```


Cheung M.C., Kan Y.W., Palek J.;
"cDNA sequence for human erythrocyte ankyrin.";
Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
[3]
VARIANT HS ILE-462.
MEDLINE=96225450; PubMed=8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyrin-1 mutations are a major cause of dominant and recessive
hereditary spherocytosis";
Nat. Genet. 13:214-218(1996).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
VARIANT 2.1.
CC -1- PTM: REGULATED BY PHOSPHORYLATION.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
HEREDITARY SPHEROCYTOSIS (HS).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; X16609; CAA34610.1; -;
EMBL; M28880; AAA51732.1; -;
PIR; S08275; SJHUK
PIR; A35049; A35049.
HSP; Q00420; IAWC.
MIM; 182900; -;
InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
InterPro; IPR000906; ZU5.
Pfam; PF00023; ank; 23.
Pfam; PF00531; death; 1.
Pfam; PF00791; ZU5; 1.
SMART; SM00248; ANK; 22.
SMART; SM00005; DEATH; 1.
SMART; SM00218; ZU5; 1.
PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REPEAT_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; tipoprotein; Multigene family; Disease mutation;
Eliptocytosis; Polymorphism.
INIT_MET 0
DOMAIN 1 826 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
BINDING DOMAIN).
DOMAIN 827 1381 62 KDA DOMAIN (SPECTRIN BINDING
DOMAIN).
DOMAIN 1382 1880 55 KDA REGULATORY DOMAIN (REGULATES
THE BINDING OF ANKYRIN TO SPECTRIN
AND THE BAND 3 PROTEIN).
REPEAT 43 72 ANK 1.
REPEAT 76 105 ANK 2.
REPEAT 109 138 ANK 3.
REPEAT 142 171 ANK 4.
REPEAT 173 200 ANK 5.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129831; PubMed=7828849;
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-kD
RT protein as potential mediators of the gamma interferon-induced cell
RT death.";
RL Genes Dev. 9:15-30(1995).
RN [2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X76104; CAA53712.1; -.
DR HSP; G63450; 1A06.
DR MIM; 600831; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000719; Ank_kinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00023; ank; 8.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00248; ANK; 7.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50088; ANK_REPEAT; 6.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT DOMAIN 13 266 PROTEIN KINASE.
FT DOMAIN 267 334 CALMODULIN-BINDING.
FT REPEAT 378 407 ANK 1.
FT REPEAT 411 440 ANK 2.
FT REPEAT 444 473 ANK 3.
FT REPEAT 478 507 ANK 4.
FT REPEAT 511 540 ANK 5.
FT REPEAT 544 573 ANK 6.
FT REPEAT 577 606 ANK 7.
FT REPEAT 610 639 ANK 8.
FT REPEAT 676 705 ANK 9.
FT REPEAT 1163 1197 ANK 10.
FT DOMAIN 1313 1397 DEATH.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9EE84811004A155B CRC64;

Query Match,

17.2%; Score 130.5; DB 1; Length 1431;

Best Local Similarity 29.1%; Pred. No. 8.6e-05;
Matches 44; Conservative 14; Mismatches 54; Indels 39; Gaps 4;
QY 8 LATAAARGVEEVRALLEAVALPNAPNSYGRRPQVMMGSR-----VAELLLHGAEPN 63
DB 483 LHCAAHGYSYVAKALCEAGCNVKNRREGTEP---LLTASARGYHDIVECLAEGADLN 539
QY 64 CADP-----ATL-----TRPVHDAAREGFLDTLVVLR 91
DB 540 ACCKDGHIALHLAVRRQMEVITLLSQGCFVDYQDRHGNTPLHVACKDGNMFIVVALCE 599
QY 92 AGARLDVRDANGRLPVDLAELGHRDVARYL 122
DB 600 ANCNDISNKYGRTPPLHLAANNGILDVRYL 630

Search completed: May 7, 2002, 12:36:42
Job time: 197 sec


```
RESULT 2
Q9EQ33 ID Q99PH0 PRELIMINARY; PRT; 157 AA.
AC Q9EQ33;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Muscarella P., Knobloch T.J., Weghorst C.M.;
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
RT Identification of Inactivating Alterations in Hamster Tumor Cell
RT Lines.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292567; AAG44950.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase.
SQ SEQUENCE 157 AA; 16635 MW; 06FD66AE6B30DCFB CRC64;

Query Match 67.1%; Score 510; DB 11; Length 157;
Best Local Similarity 68.9%; Pred. No. 5.7e-37;
Matches 102; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEILLHGA 60
Db 1 MEPSADGLARAAAGQREVEVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTPRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
Db 61 EPCNEDPATLSRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVQ 120
QY 121 YLRAAGTGRGSHARIDAEGSPDIPD 148
Db 121 YLRAAGNTPGSEPAVGTSQAQTPPEVSD 148

RESULT 3
Q99PH0 ID Q99PH0 PRELIMINARY; PRT; 144 AA.
AC Q99PH0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Muscarella P., Knobloch T.J., Weghorst C.M.;
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
RT Identification of Inactivating Alterations in Hamster Tumor Cell
RT Lines.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291598; AAG59801.1; -.
DR EMBL; AF291997; AAG59801.1; JOINED.
FT NON_TER 144
SQ SEQUENCE 144 AA; 15206 MW; 8904F9C0C316A084 CRC64;

Query Match 65.9%; Score 501; DB 11; Length 144;
```

```
Best Local Similarity 70.6%; Pred. No. 3.1e-36;
Matches 101; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEILLHGA 60
Db 1 MEPSADGLARAAAGQREVEVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTPRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
Db 61 EPCNEDPATLSRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVQ 120
QY 121 YLRAAGTGRGSHARIDAEGSPDIPD 143
Db 121 YLRAAGNTPGSEPAVGTSQAQTP 143

RESULT 4
Q9R0Z3 ID Q9R0Z3 PRELIMINARY; PRT; 159 AA.
AC Q9R0Z3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE P16 PROTEIN P16INK4A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=F344/N; TISSUE=LUNG;
RX MEDLINE=9718461; PubMed=9032263;
RA Swafford D.S., Middleton S.K., Palmisano W.A., Mikula K.J.,
RA Tesfalgzi J., Baylin S.B., Herman J.G., Belinsky S.A.;
RT "Frequent aberrant methylation of p16INK4a in primary rat lung
RT tumors.";
RL Mol. Cell. Biol. 17:1366-1374(1997).
DR EMBL; L81167; AAD48924.1; -.
DR HSSP; Q60773; IAP7.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
SQ SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAE66 CRC64;

Query Match 62.7%; Score 476.5; DB 11; Length 159;
Best Local Similarity 74.6%; Pred. No. 4.7e-34;
Matches 97; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEILLHGA 60
Db 1 MEPSADGLARAAAGQREVEVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTPRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
Db 61 DSNCEDPTLSRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVR 120
QY 121 YLR---AAAG 127
Db 121 YLRLLSSAG 130

RESULT 5
P97510 ID P97510 PRELIMINARY; PRT; 168 AA.
AC P97510; P97937;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16INK4A) (CYCLIN-
DE DEPENDENT KINASE INHIBITOR PROTEIN).
```

GN Cdkn2a OR EIALPHA OR p16INK4a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2N; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
p19ARF, is a candidate for the plasmacytoma susceptibility locus,
Pctrl.,"
RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=97179476; PubMed=9021155;
RA Herzog C.R., You M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
suppressor gene,"
RT Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-155 FROM N.A.
RC STRAIN=C57BL/6J X DBA;
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=DBA/2, AND C57BL/6;
RX MEDLINE=95380169; PubMed=7651726;
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes,"
RL Oncogene 11:635-645(1995).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=DBA/2, AND C57BL/6;
RX MEDLINE=97128829; PubMed=8973369;
RA Soloff E.V., Herzog C.R., You M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=ICR SWISS;
RX MEDLINE=97128829; PubMed=8973369;
RA Soloff E.V., Herzog C.R., You M.;
RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a
(WTS1) gene,"
RL Gene 180:213-215(1996).
RN [7]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains,"
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044336; AAC08963.1; -;
DR EMBL; U49280; AAC00052.1; -;
DR EMBL; U66087; AAB39600.1; -;
DR EMBL; U66086; AAB39600.1; JOINED.
DR EMBL; AF004588; AAB61416.1; -;
DR EMBL; U47018; AAC52987.1; -;
DR EMBL; U79628; AAD00226.1; -;
DR EMBL; U79625; AAD00223.1; -;
DR EMBL; U79627; AAD00225.1; -;
DR HSSP; P42771; IBI7.
DR MGD; MGI:104738; Cdkn2a.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.

SQ SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;
Query Match 62.6%; Score 476; DB 11; Length 168;
Best Local Similarity 63.9%; Pred. No. 5.5e-34;
Matches 99; Conservative 16; Mismatches 32; Indels 8; Gaps 2;
QY 1 MEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRPIQVMMGSAARVAEILLHGA 60
DB 1 MESADRLARAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLNLNYGA 60
QY 61 EPNCAADPATLTPRVHDAAREGEFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 61 DSNCEDEPTTFSRPVHDAAREGEFLDTLVVLRHAGARLDVRDAGRLPDLAQRGHQDIVR 120
QY 121 YLRRA-----AGGT--RGSNHARIDAAEGPSDIP 147
DB 121 YLRSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTP 155

RESULT 6
OB9088 ID O89088 PRELIMINARY; PRT; 168 AA.
AC O89088;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4A (p16INK4A TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
GN Cdkn2a OR EIALPHA OR p16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CANPT; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
p19ARF, is a candidate for the plasmacytoma susceptibility locus,
Pctrl.,"
RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=MA/M4J;
RX MEDLINE=97179476; PubMed=9021155;
RA Herzog C.R., You M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
suppressor gene,"
RL Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN=BALB/CJ AND MUS MUS POSCHIAVINUS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains,"
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044335; AAC08962.1; -;
DR EMBL; U49279; AAC00051.1; -;
DR EMBL; U79626; AAD00224.1; -;
DR HSSP; P55273; 1BD8.
DR MGD; MGI:104738; Cdkn2a.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
SQ SEQUENCE 168 AA; 17915 MW; 356A973BEAC4D167 CRC64;

Query Match 62.4%; Score 474; DB 11; Length 168;

Best Local Similarity 63.2%; Pred. No. 8.2e-34;
Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;

QY 1 MEPSADWLATAAARGVERVRALLAVALPNAENSYGRPPQVMMGSRVAEILLHLGA 60
DB 1 MESADRLARAAGQRPVDRALLAGVSPNAPNFGTPTQVMMGNVHIAALLNLNGA 60
QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRPLVDLAELGHRDVAR 120
DB 61 DSNCEPTPTFSRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRPLVDLAELGHRDVAR 120
QY 121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
DB 121 YLRAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155

RESULT 7

Q9XS51 ID Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -;
DR HSSP; P42771; 1BI7.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match 59.1%; Score 449; DB 6; Length 102;
Best Local Similarity 86.0%; Pred. No. 6.7e-32;
Matches 86; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 43 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 102
DB 1 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAGTGRGSHARIDAAEG 142
DB 61 GRLPVDLAEEGRHVDVRYLRARTGCTGSGSHTGTDGAG 100

RESULT 8

Q9TSY1 ID Q9TSY1 PRELIMINARY; PRT; 103 AA.
AC Q9TSY1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).
GN CDKN2A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE;
RA Le Chalony C., Hayes H., Frelat G., Geffrotin C.;
RT "Identification and mapping of swine CDKN2A and CDKN2B exon2
sequences.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242787; CAB65454.1; -;
DR HSSP; P42771; 1BI7.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 5D23ABCC1088DE0B CRC64;

Query Match 58.4%; Score 444; DB 6; Length 103;
Best Local Similarity 84.3%; Pred. No. 1.8e-31;
Matches 86; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 43 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 102
DB 1 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAGTGRGSHARIDAAEGPS 144
DB 61 GRLPVDLAEEGRHVDVARYLRANAGRTGGSHARSNSGEDPA 102

RESULT 9

Q9XS52 ID Q9XS52 PRELIMINARY; PRT; 86 AA.
AC Q9XS52;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -;
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9340 MW; A59FF0193290E867 CRC64;

Query Match 56.2%; Score 427; DB 6; Length 86;
Best Local Similarity 97.6%; Pred. No. 4.5e-30;
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 43 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 102
DB 1 VMMGSRVAEILLHLGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAEEGRHVDVARYLRAAG 85

RESULT 10

```

Q9GMF2
ID Q9GMF2 PRELIMINARY; PRT; 81 AA.
AC Q9GMF2;
DT 01-MAY-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Venkataraj V.S., Mayor J., Modiano J.F.;
RL "Role of p16/Ink4a in familial canine cancers.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234176; AAG01087.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 8868 MW; 0E39D8D805BEAC0F CRC64;

Query Match 53.8%; Score 409; DB 6; Length 81;
Best Local Similarity 98.8%; Pred. No. 1.5e-28;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 43 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 102
Db 1 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 60

Qy 103 GRPVDLAELHGRDVARVYL 122
Db 61 GRPVDLAELHGRDVARVYL 80

RESULT 11
Q9Z1C1
ID Q9Z1C1 PRELIMINARY; PRT; 86 AA.
AC Q9Z1C1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RL "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79637; AAD00237.1; -
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 53.7%; Score 408; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 2e-28;
Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 43 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 102
Db 1 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 60

Qy 103 GRPVDLAELHGRDVARVYLRAAG 127
Db 61 GRPVDLAELHGRDVARVYLRAAG 85

RESULT 13
Q9TSY0
ID Q9TSY0 PRELIMINARY; PRT; 86 AA.
AC Q9TSY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
GN CDKN2B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LARGE WHITE;
RA Le Chalony C., Hayes H., Frelat G., Geffrotin C.;
RL "Identification and mapping of swine CDKN2A and CDKN2B exon2
sequences.";

```

```

QY 43 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 102
Db 1 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 60

QY 103 GRPVDLAELHGRDVARVYLRAAG 127
Db 61 GRPVDLAELHGRDVARVYLRAAG 85

RESULT 12
Q9QUP0
ID Q9QUP0 PRELIMINARY; PRT; 86 AA.
AC Q9QUP0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VARIOUS STRAINS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RL "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79639; AAD00234.1; -
DR EMBL; U79636; AAD00232.1; -
DR EMBL; U79638; AAD00233.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 53.7%; Score 408; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 2e-28;
Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 43 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 102
Db 1 VMMGSAVRAEALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAM 60

QY 103 GRPVDLAELHGRDVARVYLRAAG 127
Db 61 GRPVDLAELHGRDVARVYLRAAG 85

RESULT 13
Q9TSY0
ID Q9TSY0 PRELIMINARY; PRT; 86 AA.
AC Q9TSY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
GN CDKN2B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LARGE WHITE;
RA Le Chalony C., Hayes H., Frelat G., Geffrotin C.;
RL "Identification and mapping of swine CDKN2A and CDKN2B exon2
sequences.";

```

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ242788; CAB65455.1; -
 DR HSSP; P55273; 1BD8.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 2.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 KW Kinase; Cyclin.
 FT NON_TER 1
 SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CCF9 CRC64;

Query Match 53.6%; Score 407; DB 6; Length 86;
 Best Local Similarity 92.9%; Pred. No. 2.4e-28;
 Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 43 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102
 Db 1 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60
 QY 103 GRLPVDLAEELGHRDVARYLRAAG 127
 Db 61 GRLPVDLAEELGHRDVARYLRAAG 85

RESULT 14
 OS4846 PRELIMINARY; PRT; 86 AA.
 ID O54846
 AC O54846;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
 GN CDKN2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Malumbres M., Pellicer A.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF015460; AAB94534.1; -
 DR HSSP; P55273; 1BD8.
 DR InterPro; IPR002110; ANK.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 FT NON_TER 1
 SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

Query Match 53.3%; Score 405; DB 11; Length 86;
 Best Local Similarity 91.8%; Pred. No. 3.6e-28;
 Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 43 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102
 Db 1 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60
 QY 103 GRLPVDLAEELGHRDVARYLRAAG 127
 Db 61 GRLPVDLAEELGHRDVARYLRAAG 85

RESULT 15
 Q921C2 PRELIMINARY; PRT; 113 AA.
 ID Q921C2
 AC Q921C2;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
 GN P16.
 OS Mus spretus (Western wild mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRET/EI;
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
 RA Pellicer A., Fernandez-Piqueras J.;
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
 in mouse inbred strains.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79634; AAD00236.1; -
 DR HSSP; P55273; 1BD8.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 2.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 KW Kinase; Cyclin.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;

Query Match 43.9%; Score 334; DB 11; Length 113;
 Best Local Similarity 61.1%; Pred. No. 7.1e-22;
 Matches 69; Conservative 12; Mismatches 24; Indels 8; Gaps 2;
 QY 43 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102
 Db 1 VMMGSAARVAELLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60
 QY 103 GRLPVDLAEELGHRDVARYLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
 Db 61 GRLPVDLAEELGHRDVARYLRAA-----AGGT--RGSNHARIDAAEGPSDIP 113

Search completed: May 7, 2002, 12:36:23
 Job time: 193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:49 ; Search time 23.63 Seconds
(without alignments)
463.938 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760
Sequence: 1 MEPSADNLATAAARGRVEEV.....TRGSNHNARIDAERGSPDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	16 AAR81701	Multiple tumour su
2	760	100.0	148	16 AAR80940	Human multiple tum
3	760	100.0	151	15 AAR53401	Inhibitor of cycli
4	760	100.0	156	16 AAR85116	Cell-cycle regulat
5	760	100.0	156	20 AAY24741	Human INK-4 protei
6	760	100.0	156	21 AAY88354	Human cell cycle r
7	760	100.0	391	18 AAW23534	CDK inhibitory fus
8	760	100.0	391	20 AAW95094	Human p27-pl6 fusi
9	760	100.0	391	21 AAY97526	Human W3 protein s
10	760	100.0	391	21 AAY96041	Antiproliferative
11	760	100.0	391	21 AAY96068	Angiogenesis inhib

12	753	99.1	156	18 AAW10627	Tumour suppressor
13	753	99.1	156	18 AAW19251	Human multiple tum
14	753	99.1	156	19 AAW74549	Amino acid sequenc
15	753	99.1	156	19 AAW40524	Human WTS1 protein
16	753	99.1	156	20 AAW80524	A human multiple t
17	753	99.1	156	21 AAB15498	Human WTS1 protein
18	753	99.1	156	21 AAY97524	Human p16 protein
19	753	99.1	156	21 AAY96053	Human cyclin depen
20	753	99.1	156	21 AAY96067	Human cyclin depen
21	753	99.1	156	21 AAY92921	Human multiple tum
22	753	99.1	156	21 AAY91102	Human multiple tum
23	753	99.1	156	21 AAY59415	Human WTS1 protein
24	753	99.1	156	21 AAY54902	Human multiple tum
25	753	99.1	156	22 AAO02122	Human multiple tum
26	753	99.1	156	22 AAE01002	Human multiple tum
27	753	99.1	156	22 AAB67334	Protein encoded by
28	753	99.1	156	22 AAB36890	Human Multiple Tum
29	753	99.1	228	21 AAY97522	Human W9 protein s
30	753	99.1	228	21 AAY96051	Antiproliferative
31	753	99.1	228	21 AAY96078	Angiogenesis inhib
32	753	99.1	237	20 AAW95105	Truncated p27/pl6
33	753	99.1	237	21 AAY97534	Human W9 protein s
34	753	99.1	237	21 AAY96049	Antiproliferative
35	753	99.1	237	21 AAY96076	Angiogenesis inhib
36	753	99.1	252	20 AAW95106	Truncated p27/pl6
37	753	99.1	252	21 AAY97535	Human W10 protein
38	753	99.1	252	21 AAY96050	Antiproliferative
39	753	99.1	252	21 AAY96077	Angiogenesis inhib
40	753	99.1	323	21 AAY96079	Secretable angio
41	753	99.1	334	20 AAW95103	Truncated p27/pl6
42	753	99.1	334	21 AAY97532	Human W8 protein s
43	753	99.1	334	21 AAY96047	Antiproliferative
44	753	99.1	334	21 AAY96074	Angiogenesis inhib
45	753	99.1	365	18 AAW23536	CDK inhibitory fus

ALIGNMENTS

RESULT 1
AAR81701
ID AAR81701 standard; Protein; 148 AA.
XX
AC AAR81701;
XX
DT 08-MAY-1996 (first entry)
XX
DE Multiple tumour suppressor 1 (MTS1) polypeptide.
XX
DE Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid.
XX
OS Homo sapiens.
XX
PN WO9525813-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US03537.
XX
PR 01-JUN-1994; 94US-0251938.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Cannon-Albright LA, Kamb A, Skolnick MH;
XX
DR WPI; 1995-344626/44.

DR N-PSDB; AAT00736.
XX
PT Detecting polymorphism associated with cancer pre-disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
XX
PS Example 8; Pages 92-93; 148pp; English.
XX
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1
CC gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.
CC The above assay can also be used in the diagnosis and prognosis of
CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CC cancers, etc..
XX
SQ Sequence 148 AA;

Query Match 100.0%; Score 760; DB 16; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVMMGMSARVAELLLHGA 60
Db 1 mepsadwlataaargveevrallleavalpnapsygrpiqvmmsarvaeillllhga 60

QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEEELGHRDVAR 120
Db 61 epncadpatltrpvhdaaregfdtlvvlhragardlvrdawgripvdlaeelghrdvar 120

QY 121 YLRAAAGGTRGSHARIDAAGPSDIPD 148
Db 121 ylr aaaggtrgsnharidaaegpsdipd 148

RESULT 2
ID AAR80940 standard; Protein; 148 AA.
XX AAR80940;
XX
DT 03-MAY-1996 (first entry)
XX
DE Human multiple tumour suppressor polypeptide, MTS1.
XX
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW gene therapy; chronic.
XX
OS Homo sapiens.
XX
PN WO9525429-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US03316.
XX
PR 01-JUN-1994; 94US-0251938.
PR 18-MAR-1994; 94US-0214581.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215088.
PR 14-APR-1994; 94US-0227369.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Kamb A;
XX
DR WPI; 1995-344401/44.
DR N-PSDB; AAQ99158.
XX

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
XX
PS Claim 5; Page 92-93; 156pp; English.
XX
CC Several multiple tumour suppressor (MTS) polypeptides have been
CC isolated and sequenced. This sequence is the MTS polypeptide MTS1
CC MTS polypeptide-encoding cDNAs and mutants of these are useful for
CC the diagnosis or prognosis of human cancer. Germ-line mutations of
CC MTS cDNAs can be used for diagnosing predisposition to melanoma,
CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,
CC testis, kidney, stomach and rectum. The wild-type gene is useful
CC for gene therapy and MTS polypeptides may also be used for protein
CC replacement therapy. Also the polypeptides or cells contg. an
CC altered MTS gene are useful for screening for potential cancer
CC therapeutics.
XX
SQ Sequence 148 AA;

Query Match 100.0%; Score 760; DB 16; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVMMGMSARVAELLLHGA 60
Db 1 mepsadwlataaargveevrallleavalpnapsygrpiqvmmsarvaeillllhga 60

QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEEELGHRDVAR 120
Db 61 epncadpatltrpvhdaaregfdtlvvlhragardlvrdawgripvdlaeelghrdvar 120

QY 121 YLRAAAGGTRGSHARIDAAGPSDIPD 148
Db 121 ylr aaaggtrgsnharidaaegpsdipd 148

RESULT 3
ID AAR53401 standard; Protein; 151 AA.
XX AAR53401;
XX
DT 07-DEC-1994 (first entry)
XX
DE Inhibitor of cyclin dependent kinase 4 (p16INK4).
XX
KW Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;
KW lymphoma; cell cycle; detection; identification; tumour virus;
KW proliferating cell nuclear antigen; subunit; complex.
XX
OS Homo sapiens.
XX
PN WO9409135-A.
XX
PD 28-APR-1994.
XX
PF 18-OCT-1993; 93WO-US09945.
XX
PR 16-OCT-1992; 92US-0963308.
PR 17-DEC-1992; 92US-0991997.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Beach DH, Xiong Y;
XX
DR WPI; 1994-151320/18.
DR N-PSDB; AAQ63491.
XX
PT Detection of subunit components of cyclin complexes - used for
PT diagnosing transformation of a cell and developing inhibitors and

PT activators, partic for cancer treatment

PS Claim 13; Page 40; 45pp; English.

XX The cell cycle gene implicated most strongly in oncogenesis is the
 CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a
 CC locus activated by translocation to an immunoglobulin gene enhancer
 CC in some B-cell lymphomas and leukaemias. D-type cyclin, cyclin
 CC dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and
 CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many
 CC combinatorial variations of the components e.g. cyclin D1 or D3 and
 CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may
 CC have a subtly different role in the cell cycle or in different cell
 CC types. Cellular transformation by DNA tumour viruses such as SV40
 CC is associated with selective subunit rearrangement of the cyclin D
 CC complexes. In virally transformed cells, CDK4 totally dissociates
 CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton
 CC polypeptide (p16). This sequence, designated p16INK4, binds to and
 CC inhibits CDK4. p16INK4 was discovered to show many similarities to
 CC p16. Reagents, such as monoclonal antibodies, can be developed that
 CC recognise the interactions between the CDK's cyclins, PCNA and low
 CC molecular weight polypeptides and can therefore be used to identify
 CC the state of transformation of a cell.

XX Sequence 151 AA;

Query Match 100.0%; Score 760; DB 15; Length 151;

Best Local Similarity 100.0%; Pred. No. 4.5e-83; Indels 0; Gaps 0;

Matches 148; Conservative 0; Mismatches 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPIQVMMGMSARVAEILLHGA 60
 DB 1 mepsadwlataaargveevrllleavlpnapnsygrpiqvmgmsarvaeillhga 60
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRAGRLPVDLAEEIGHRDVAR 120
 DB 61 epncadpatltrpvhdaaregfdtlvvlrhagardlvdragrlpvdlaeelghrdvar 120
 QY 121 YLRAAGGTGRGSHARIDAEGPSDIPD 148
 DB 121 ylrraaggtgrgsharidaegpsdipd 148

RESULT 4

AAR85116
 ID AAR85116 standard; Protein; 156 AA.

AC AAR85116;

DT 01-MAR-1996 (first entry)

XX Cell-cycle regulatory protein p16.

XX Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
 KW CCR; cancer; cell proliferation.

XX Homo sapiens.

XX W09528483-A1.

XX 26-OCT-1995.

XX 14-APR-1995; 95WO-US04636.

XX 29-NOV-1994; 94US-0346147.

XX 14-APR-1994; 94US-0227371.

XX 25-MAY-1994; 94US-0248812.

XX 14-SEP-1994; 94US-0306511.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Beach DH, Demetrick DJ, Hannon GJ, Serrano M;

PI WPI; 1999-394656/33.

XX

DR WPI: 1995-373798/48.

DR N-PSDB; AAT02962.

XX

PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 CC and related nucleic acids, antibodies etc., used in diagnosis and
 CC therapy of abnormal cell proliferation, degeneration etc.

PS Claim 1; Page 76-77; 109pp; English.

XX

CC The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was
 CC obtd. by expression of a cDNA clone (AAT02962) isolated in a 2-hybrid
 CC screening assay. CCR p16 specifically inhibits the activity of
 CC cyclin-dependent kinases during various stages of the cell cycle,
 CC and can be used in the treatment and diagnosis of proliferative
 CC disorders.

XX Sequence 156 AA;

Query Match 100.0%; Score 760; DB 16; Length 156;

Best Local Similarity 100.0%; Pred. No. 4.7e-83; Indels 0; Gaps 0;

Matches 148; Conservative 0; Mismatches 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPIQVMMGMSARVAEILLHGA 60
 DB 9 mepsadwlataaargveevrllleavlpnapnsygrpiqvmgmsarvaeillhga 68
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRAGRLPVDLAEEIGHRDVAR 120
 DB 69 epncadpatltrpvhdaaregfdtlvvlrhagardlvdragrlpvdlaeelghrdvar 128
 QY 121 YLRAAGGTGRGSHARIDAEGPSDIPD 148
 DB 129 ylrraaggtgrgsharidaegpsdipd 156

RESULT 5

AAY24741

ID AAY24741 standard; Protein; 156 AA.

AC AAY24741;

DT 23-AUG-1999 (first entry)

XX Human INK-4 protein p16.

XX INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein;

KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.

XX Homo sapiens.

XX US5919997-A.

XX 06-JUL-1999.

XX 04-APR-1996; 96US-0627610.

XX 04-APR-1996; 96US-0627610.

XX 18-NOV-1993; 93US-0154915.

XX 14-APR-1994; 94US-0227371.

XX 25-MAY-1994; 94US-0248812.

XX 14-SEP-1994; 94US-0306511.

XX 29-NOV-1994; 94US-0346147.

XX 30-JUN-1995; 95US-0497214.

XX 02-JAN-1996; 96US-0581918.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

XX Beach DH, DePinho RA, Serrano M;

DR WPI; 1999-394656/33.

DR N-PSDB; AAX80472.
XX Transgenic mice with modified cell-cycle regulation
PS Disclosure; Column 45-46; 35pp; English.
XX
CC The present invention describes a transgenic mouse having germline and
CC somatic cells which comprise an incorporated transgene that disrupts and
CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also
CC described is a method of making a mouse and mouse embryonic stem cells a
CC functionally disrupted p16-INK4-a gene which comprises transferring a
CC transgene construct into embryonic stem cells of a mouse and
CC transferring these into a mouse blastocyst and implanting the resulting
CC chimeric blastocyst into a female mouse selecting offspring having an
CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for
CC evaluating the carcinogenic potential or the anti-proliferative activity
CC of a test compound. The present sequence represents the human INK4
CC protein p16 given in the present invention.
XX
SQ Sequence 156 AA;

Query Match 100.0%; Score 760; DB 20; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.7e-83; Indels 0; Gaps 0;
Matches 148; Conservative 0; Mismatches 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVAELLLHGA 60
DB 9 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVAELLLHGA 68

QY 61 EPNCAADPATLTPRVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDVAR 120
DB 69 EPNCAADPATLTPRVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAAGPSDIPD 148
DB 129 YLRAAAGTGRGSHARIDAAGPSDIPD 156

QY 121 YLRAAAGTGRGSHARIDAAGPSDIPD 148
DB 129 YLRAAAGTGRGSHARIDAAGPSDIPD 156

RESULT 6
AAX88354
ID AAX88354 standard; Protein; 156 AA.
XX
AC AAX88354;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human cell cycle regulatory protein p16 amino acid sequence.
XX
KW Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;
KW cell proliferation; differentiation; neoplasia; cancer; cell growth;
KW cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
XX
OS Homo sapiens.
XX
PN US6043030-A.
XX
PD 28-MAR-2000.
XX
PF 02-JAN-1996; 96US-0581918.
XX
PR 17-DEC-1992; 92US-0991997.
PR 18-NOV-1993; 93US-0154915.
PR 14-APR-1994; 94US-0227371.
PR 25-MAY-1994; 94US-0248812.
PR 14-SEP-1994; 94US-0306511.
PR 29-NOV-1994; 94US-0346147.
PR 30-JUN-1995; 95US-0497214.
XX
(COLD-) COLD SPRING HARBOR LAB.
PA Beach DH, Demetrick DJ, Serrano M, Hannon GJ;
PI
XX

DR WPI; 2000-270336/23.
XX N-PSDB; AAA13096.
XX
PT Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory
PT protein) in a diagnostic assay for identifying a cell at risk for a
PT disorder characterized by unwanted cell proliferation or
PT differentiation -
XX
PS Claim 14; Column 57-58; 61pp; English.
XX
CC This sequence represents the human cell cycle regulatory protein (CCR)
CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.
CC The invention relates to a diagnostic assay which comprises detecting a
CC mutation in the p16 gene, which is used to identify a cell or cells at
CC risk of developing a disorder characterised by unwanted cell
CC proliferation or differentiation. p16 is a cyclin-dependent kinase
CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle
CC progression and ultimately cell growth. The assay can be used for
CC identifying a cell or cells at risk for a disorder (neoplasia)
CC characterized by unwanted cell proliferation or differentiation. The
CC method is used for detecting mutations in either a CCR gene or CDK gene
CC which alter complex formation between these two proteins. The method is
CC also used for detecting mutations in other cellular proteins which
CC disrupt protein interactions such as mutations which disrupt binding of
CC the p33 protein with other cellular proteins, e.g. Wilms' tumour
CC suppressor protein WT1. They can also be used to detect mutations in
CC pairs of signal transduction proteins such as ras protein or other
CC cellular proteins which interact with ras, e.g. ras GTPase activating
CC proteins (GAPs). The method is convenient for detecting mutants of CCR
CC genes encoding proteins which are unable to physically interact with a
CC CDK bait protein.
XX
SQ Sequence 156 AA;

Query Match 100.0%; Score 760; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.7e-83; Indels 0; Gaps 0;
Matches 148; Conservative 0; Mismatches 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVAELLLHGA 60
DB 9 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVAELLLHGA 68

QY 61 EPNCAADPATLTPRVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDVAR 120
DB 69 EPNCAADPATLTPRVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAAGPSDIPD 148
DB 129 YLRAAAGTGRGSHARIDAAGPSDIPD 156

RESULT 7
AAW23534
ID AAW23534 standard; Protein; 391 AA.
XX
AC AAW23534;
XX
DT 16-MAR-1998 (first entry)
XX
DE CDK inhibitory fusion protein #1.
XX
KW Fusion gene; CDK inhibitor; cyclin-dependent kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..7
FT Misc-difference /note= "poly-His tag"
FT Misc-difference 205..219

/note= "(Gly4Ser)2 linker"

FT XX W09727297-A1.
 FN XX
 PD XX 31-JUL-1997.
 XX XX
 PF XX 17-JAN-1997; 97WO-US00369.
 XX XX
 PR XX 23-JAN-1996; 96US-0589981.
 XX XX
 PA (MITO-) MITOTIX INC.
 XX XX
 PI Beach D, Gyuris J, Lamphere L;
 XX XX
 DR WPI; 1997-393685/36.
 XX XX
 DR N-PSDB; AAT74051.
 XX XX
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
 PT therapy of cancer and other proliferative and differentiative
 PT diseases
 XX XX
 PS Claim 40; Page 38-40; 58pp; English.
 XX XX
 CC This sequence represents a chimeric polypeptide of the invention. It was
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The
 CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
 CC binding motifs from at least two different proteins that bind to CDKs.
 CC The protein controls proliferation and/or differentiation of cells,
 CC particularly they inhibit cell-cycle progression. They can be used to
 CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
 CC can also treat diseases associated with de-differentiation or
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
 CC diseases, gastric ulcers and autonomous diseases of the peripheral
 CC nervous system. Other applications include reducing growth of hair and
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain
 CC cells, especially neurons intended for testing specific activity of
 CC trophic factors, at selected points in the cell cycle. The proteins are
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used
 CC individually (since they may bind to CDK involved in different stages of
 CC the cell cycle).
 XX XX
 SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 18; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60
 |||||||
 Db 244 mepsadwlataaargrveevrllleavalpnapsygrrrpqvmmgmsarvae||llhga 303
 |||||||

Qy 61 EPNCADPATLRPVHDAARSGFDLTLLVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
 |||||||
 Db 304 epncadpatlrrpvhdarsgfdltllvlrhtagarldvdrdagrplvdlaeelghrdvar 363
 |||||||

Qy 121 YLRAAAGTGRCSNHARIDAAEGPSDIPD 148
 |||||||
 Db 364 ylraaagtgrcsnharidaaegpsdipd 391
 |||||||

RESULT 8
 AAW95094
 ID AAW95094 standard; Protein; 391 AA.
 XX
 AC AAW95094;
 XX
 DT 25-MAY-1999 (first entry)
 XX
 DE Human p27-p16 fusion protein.

XX
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16.
 XX
 OS Homo sapiens.
 XX
 PN W09906540-A2.
 XX
 XX 11-FEB-1999.
 XX
 PF 29-JUL-1998; 98WO-US15759.
 XX
 PR 29-JUL-1997; 97US-0902572.
 XX
 XX (MITO-) MITOTIX INC.
 PA
 XX Beach DH, Gyuris J, Lamphere L;
 PI
 XX WPI; 1999-153770/13.
 DR
 DR N-PSDB; AAX26220.
 XX
 CC Fusion and chimaeric proteins including cyclin-dependent kinase
 CC binding motif - used for regulation of cell proliferation and
 CC differentiation, for treatment of, e.g. vascular injury, cancers,
 CC fibrosis and neurodegeneration
 PT
 PT
 PT
 XX
 PS Claim 63; Page 70-72; 88pp; English.
 XX
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCS to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. (A) are used to
 CC treat vascular wounds that involve a break in the endothelium and
 CC excessive proliferation of smooth muscle, particularly restenosis but
 CC more generally any repair of cardiovascular damage, arteriosclerotic
 CC lesions or for endothelialisation of synthetic vascular grafts. More
 CC generally, FP are used to treat unwanted cellular proliferation in a very
 CC wide range of situations, e.g. for treating vascular diseases as above;
 CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many
 CC tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration;
 CC acne; also to control hair growth (e.g. to prevent hair loss caused by
 CC chemotherapy or radiation); periodontal disease; to treat tachycardia;
 CC to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding
 CC motifs from two or more different proteins bind to CDKs so inhibit cell
 CC cycle progression, particularly smooth muscle cell proliferation. The
 CC gene constructs may also be used to produce FP in cell cultures, for
 CC production or for regulating cell differentiation in vitro. The present
 CC sequence represents a human p27-p16 fusion protein.
 XX
 SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 20; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60
 |||||||

Db 244 mepsadwlataaargrveevrallleavalpnapsygrrrpqvmummgarvaeallllhga 303
QY 61 EPCNADPATLTRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAELGHRDVAR 120
|||||
Db 304 epcnadcpatlrvphdaaregfdltlvllhrragardlrvdawgrlvpvdlaeelghrdvar 363
QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
|||||
Db 364 yltraaagtrgsharidaaegpsdipd 391
RESULT 9
AA97526
ID AAY97526 standard; Protein; 391 AA.
XX
AC AAY97526;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human W3 protein sequence.
XX
KW Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy;
KW adenovirus E4 protein; neoplasia; W3 protein.
XX
OS Homo sapiens.
XX
FN WO200052184-A1.
PN
XX
PD 08-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US05350.
XX
PR 01-MAR-1999; 99US-0122974.
PR 08-APR-1999; 99US-0128271.
PR 09-APR-1999; 99US-0128515.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
DR WPI: 2000-587315/55.
DR N-PSDB; AA90923.
XX
PT Protein and nucleic acid compositions for preventing and treating
PT neoplasias (particularly cancer), comprises a novel chimeric cyclin
PT dependent kinase inhibitor and adenovirus E4 protein -
XX
PS Example 1; Page 108-109; 126pp; English.
XX
CC This sequence represents the human W3 protein.
CC The invention relates to a protein composition comprising a novel
CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
CC purified adenovirus E4 protein. The compositions comprising the protein,
CC or the DNA encoding it are useful for treating neoplasias in animals. The
CC compositions also find use in assays to eliminate a specific
CC sub-population of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronise cell growth in cultured cells.
XX
SQ Sequence 391 AA;
Query Match 100.0%; Score 760; DB 21; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-82;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGRVEEVRRALLEVALPNAPSNYGRRRPQVMMMGARVAELLLLHGA 60
Db 244 mepsadwlataaargrveevrallleavalpnapsygrrrpqvmummgarvaeallllhga 303
QY 61 EPCNADPATLTRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAELGHRDVAR 120
|||||

Db 304 epcnadcpatlrvphdaaregfdltlvllhrragardlrvdawgrlvpvdlaeelghrdvar 363
QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
|||||
Db 364 yltraaagtrgsharidaaegpsdipd 391
RESULT 10
AA96041
ID AAY96041 standard; Protein; 391 AA.
XX
AC AAY96041;
XX
DT 05-DEC-2000 (first entry)
XX
DE Antiproliferative p27-pl6 fusion protein W3.
XX
KW Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4;
KW p16; human; smooth muscle cell; hyperproliferation; restenosis;
KW vasotropic; antiproliferative; gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN Key Location/Qualifiers
FT Peptide 1..7
FT Protein /label= 6His_tag
FT Protein 8..204
FT Peptide /label= p27
FT Peptide 205..219
FT Protein /label= Hinge
FT Protein 239..391
FT Protein /label= p16
XX
PN WO200052159-A1.
XX
PD 08-SEP-2000.
XX
PF 28-FEB-2000; 2000WO-US04971.
XX
PR 01-MAR-1999; 99US-0122974.
PR 05-NOV-1999; 99US-0163682.
PR 09-DEC-1999; 99US-0457568.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI McArthur J, Gyuris J, Finer M;
DR WPI: 2000-594183/56.
DR N-PSDB; AAA50488.
XX
PT Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
PS Example 1; Page 101-103; 126pp; English.
XX
CC The present sequence is that of p27-pl6 fusion protein W3 comprising
CC an N-terminal 6His tag, the human p27 protein (see AAY96052), a
CC (Gly4Ser)3 hinge and the human p16 protein (see AAY96053). It is
CC encoded by a nucleic acid obtained by PCR amplification of p27 and
CC p16 DNAs using primers that also included codons for the tag/hinge
CC regions. A claimed method for inhibiting smooth muscle cell
CC hyperproliferation involves transducing smooth muscle cells with a
CC replication-deficient recombinant adenovirus that lacks functional
CC E1 and E4 regions, and comprises a transgene encoding a cyclin
CC dependent kinase inhibitor (CDKi). The CDKi is selected from an
CC INK4 family protein such as human p16, a CIP/KIP family protein
CC such as p27, active fragments of these, or fusion proteins
CC comprising (active fragments of) an INK4 family protein and a
CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used
CC to inhibit mammalian smooth muscle cell hyperproliferation, induced

CC by injury caused by angioplasty, stent placement or vein
 CC engraftment. It is useful for treating vascular pathologies e.g.,
 CC restenosis. Also claimed are recombinant lentiviruses encoding
 CC CDKis.
 XX
 SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 21; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVREALLAEVALPNAPNSYGRRPQVMMGMSARVAELLHLHGA 60
 DB 244 mepsadwlataaargveevreallaevalpnapsygrripqvmmsarvaeallhlhga 303
 QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120
 DB 304 epncadpatltprvhdaaregfdltvlvhragarldvdragrldpvdlaeeighrdvar 363
 QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
 DB 364 yltraaagtgrgsharidaaegpsdipd 391

RESULT 11
 AAY96068
 ID AAY96068 standard; Protein; 391 AA.
 AC AAY96068;
 DT 05-DEC-2000 (first entry)
 DE Angiogenesis inhibitor (p27-p16 fusion) W3.
 XX
 KW Cyclin dependent kinase inhibitor; CDK; CIP; KIP; INK4; p27; p16;
 KW human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;
 KW antiproliferative; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH Peptide 1..7
 FT /label= 6His_tag
 FT Protein 8..204
 FT /label= p27
 FT Peptide 205..219
 FT /label= Hinge
 FT Protein 239..391
 FT /label= p16
 XX
 PN WO200052158-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 28-FEB-2000; 2000WO-US04970.
 XX
 PR 01-MAR-1999; 99US-0122974.
 PR 05-NOV-1999; 99US-0163682.
 PR 09-DEC-1999; 99US-0457646.
 XX
 PA (CELL-) CELL GENESYS INC.
 PA (MITO-) MITOTIX INC.
 XX
 PI Patel S, McArthur J, Gyuris J;
 XX
 DR WPI; 2000-565501/52.
 DR N-PSDB; AAA50523.
 XX
 PT Inhibiting angiogenesis and treating angiogenesis-associated

PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial
 PT cell with a recombinant virus having a transgene encoding a cyclin
 XX dependent kinase inhibitor
 PS Example 1; Page 108-110; 138pp; English.
 XX
 CC The present sequence is that of p27-p16 fusion protein W3
 CC comprising an N-terminal 6His tag, the human p27 protein (see
 CC AAY96068), a (Gly4Ser)3 hinge, and the human p16 protein (see
 CC AAY96067). The fusion protein is encoded by a nucleic acid (see
 CC AAA50523) that was obtained by PCR amplification of human p27 and p16
 CC DNAs using primers that also included codons encoding the tag/hinge
 CC regions of the fusion protein. A claimed method for inhibiting
 CC angiogenesis involves transducing an epithelial cell with a
 CC transgene encoding a cell dependent kinase inhibitor (CDK). The
 CC delivery system for the transgene is a liposome or a recombinant
 CC virus. The CDK is a protein of the CIP/KIP family such as p27, a
 CC protein of the INK4 family such as p16, active fragments of these
 CC proteins, or a fusion of 2 CDK proteins such as p27 and p16. The
 CC method is useful in treating conditions associated with angiogenesis,
 CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis
 CC and vascular retinopathy (claimed). Alternatively, the transgene
 CC is delivered to an auxiliary cell, and is expressed by that cell
 CC such that the CDK is released into the blood and contacts the
 CC target epithelial cell. The p27-p16 fusion proteins interact with
 CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
 CC progression.
 XX
 SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 21; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVREALLAEVALPNAPNSYGRRPQVMMGMSARVAELLHLHGA 60
 DB 244 mepsadwlataaargveevreallaevalpnapsygrripqvmmsarvaeallhlhga 303
 QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120
 DB 304 epncadpatltprvhdaaregfdltvlvhragarldvdragrldpvdlaeeighrdvar 363
 QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
 DB 364 yltraaagtgrgsharidaaegpsdipd 391

RESULT 12

AAW10627
 ID AAW10627 standard; Protein; 156 AA.

XX AAW10627;

XX 28-OCT-1997 (first entry)

XX Tumour suppressor p16.

XX Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
 KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
 KW anti-angiogenic activity; hyperproliferative disorder.

XX Homo sapiens.

XX WO9703635-A2.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-US11787.

XX 17-JUL-1995; 95US-0502881.

XX (TEXA) UNIV TEXAS SYSTEM.

```

XX Jin X, Roth J;
PI WPI: 1997-132336/12.
DR N-PSDB; AAT60951.
XX
XX Expression construct contg. DNA for tumour suppressor p16 - to
PT restore p16 activity to transformed cells, useful for treating lung
PT or bladder cancer or melanoma
XX
XX Disclosure; Fig 1b; 92pp; English.
XX
XX This sequence represents the tumour suppressor p16. The DNA encoding
CC this sequence is joined to a promoter functional in eukaryotic cells and
CC used in the expression construct of the invention. p16 is an inhibitory
CC subunit, which is involved in the control of cyclin-dependent kinase 4
CC activity, and functions as a tumour suppressor. By detecting this
CC sequence or the DNA encoding it, cancer cells can be detected. When the
CC nucleic acid molecule is in the sense orientation, the expression
CC construct can be used to restore p16 function in a cell, particularly by
CC reversing the transformed phenotype in tumours, especially lung or
CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
CC nucleic acid molecule is inserted in the antisense orientation, the
CC expression construct inhibits p16 function. Reduced or increased levels
CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
CC or immunoassay.
XX
XX Sequence 156 AA;
SQ

```

Query Match 99.1%; Score 753; DB 18; Length 156;
Best Local Similarity 99.3%; Pred. No. 3.3e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60
DB 9 mepsadwlataaargveevrallleesgalpnapsygrrrpigmmsgsarvae11llhga 68
QY 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEEIGHRDVAR 120
DB 69 epcncadpatltpvhdaaregfltdltvlvhragarlvdvrdawgripvdlaeelghrdvar 128
QY 121 YLRAAAGGTGSGNHARIDAAEGPSDIPD 148
DB 129 ylraaaggtgrgsharidaaegpsdipd 156

```

RESULT 13
AAW19251
ID AAW19251 standard; Protein; 156 AA.
XX
XX AAW19251;
XX
XX 10-SEP-1997 (first entry)
XX
XX Human multiple tumour suppressor 1 gene product.
XX
XX Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
XX
XX Homo sapiens.
XX
XX US5624819-A.
XX
XX 29-APR-1997.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 07-JUN-1995; 95US-0474177.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.

```

PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03537.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
XX
XX Cannon-Albright LA, Kamb A, Skolnick MH;
XX
XX WPI: 1997-258217/23.
DR N-PSDB; AAT72311.
XX
XX Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
XX
XX Claim 1; Columns 61-64; 72pp; English.
XX
XX The present sequence the human multiple tumour suppressor 1
CC (MTS1) gene product, useful in cancer diagnosis.
CC
XX Sequence 156 AA;
SQ

```

Query Match 99.1%; Score 753; DB 18; Length 156;
Best Local Similarity 99.3%; Pred. No. 3.3e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60
DB 9 mepsadwlataaargveevrallleesgalpnapsygrrrpigmmsgsarvae11llhga 68
QY 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEEIGHRDVAR 120
DB 69 epcncadpatltpvhdaaregfltdltvlvhragarlvdvrdawgripvdlaeelghrdvar 128
QY 121 YLRAAAGGTGSGNHARIDAAEGPSDIPD 148
DB 129 ylraaaggtgrgsharidaaegpsdipd 156

```

RESULT 14
AAW74549
ID AAW74549 standard; Protein; 156 AA.
XX
XX AAW74549;
XX
XX 04-DEC-1998 (first entry)
XX
XX Amino acid sequence of multiple tumour suppressor 1.
XX
XX Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
XX
XX Homo sapiens.
XX
XX US5801236-A.
XX
XX 01-SEP-1998.
XX
XX 07-JUN-1995; 95US-0480810.
XX
XX 07-JUN-1995; 95US-0480810.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.
XX
XX 14-APR-1994; 94US-0227369.
XX
XX 01-JUN-1994; 94US-0251938.
XX
XX 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX

DR WPI; 1998-494842/42.
 DR N-PSDB; AAV53819.
 XX
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 PT useful as hybridisation probes, primers and recombinant production
 PT of MTS in the diagnosis and treatment of cancers related to MTS
 PT mutation(s)
 XX
 PS Disclosure; Column 63-64; 73pp; English.
 XX
 CC This is the amino acid sequence of the multiple tumour suppressor 1
 CC (MTS-1) protein, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic acid hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations
 CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.
 XX
 SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 19; Length 156;
 Best Local Similarity 99.3%; Pred. No. 3.3e-82;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQYMMMGSAARVAELLLHGA 60
 Db 9 mepsadwlataaargveevrllleagalpnapsygrripqymmmgsarvaeillllhga 68
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEEELGHRDVAR 120
 Db 69 epncadpatltrpvhdaaregfdtlvvlrhagarldvrdawgrlpvdlaeelghrdvar 128
 QY 121 YLRAAAGGTGRGSHNARIDAAEGPSDIPD 148
 Db 129 ylr aaaggtrgshnaridaaegpsdipd 156

RESULT 15
 AAW40524
 ID AAW40524 standard; Protein; 156 AA.
 XX
 AC AAW40524;
 XX
 DT 15-JUL-1998 (first entry)
 XX
 DE Human MTS1 protein.
 XX
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
 KW familial melanoma locus; MLM; predisposition.
 XX
 OS Homo sapiens.
 XX
 PN U55739027-A.
 XX
 PD 14-APR-1998.
 XX
 PF 07-JUN-1995; 95US-0487033.
 XX
 PR 07-JUN-1995; 95US-0487033.
 PR 18-MAR-1994; 94US-0214582.
 PR 18-MAR-1994; 94US-0215086.
 PR 18-MAR-1994; 94US-0215087.
 PR 14-APR-1994; 94US-0227369.
 PR 01-JUN-1994; 94US-0251938.
 PR 17-MAR-1995; 95WO-US03316.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;
 PI
 XX
 DR WPI; 1998-250421/22.
 DR N-PSDB; AAV11238.
 XX
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
 PT useful for the diagnosis of cancers related to MTS1E1-beta
 PT mutation(s) and their treatment
 XX
 PS Disclosure; Column 63-64; 72pp; English.
 XX
 CC This sequence represents a human multiple tumour suppression protein,
 CC MTS1. The MTS gene locus is also referred to as the familial melanoma
 CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
 CC in MTS genes can be used in the diagnosis of predisposition to cancers,
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
 CC ovary, uterus, testis, kidney, stomach and rectum.
 XX
 SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 19; Length 156;
 Best Local Similarity 99.3%; Pred. No. 3.3e-82;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQYMMMGSAARVAELLLHGA 60
 Db 9 mepsadwlataaargveevrllleagalpnapsygrripqymmmgsarvaeillllhga 68
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEEELGHRDVAR 120
 Db 69 epncadpatltrpvhdaaregfdtlvvlrhagarldvrdawgrlpvdlaeelghrdvar 128
 QY 121 YLRAAAGGTGRGSHNARIDAAEGPSDIPD 148
 Db 129 ylr aaaggtrgshnaridaaegpsdipd 156

Search completed: May 7, 2002, 12:33:04
 Job time: 555 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:10 ; Search time 105.99 Seconds
(without alignments)
490.476 Million cell updates/sec

Title: US-09-016-869B-35
Perfect score: 760
Sequence: 1 MEPSADMLATAAARGVEEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US60_MERGED_COMB.pep1.*
26: /cgn2_6/ptodata/2/paa/US10_MERGED_COMB.pep1.*
27: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep2.*
28: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep1.*
29: /cgn2_6/ptodata/2/paa/US08_MERGED_COMB.pep1.*
30: /cgn2_6/ptodata/2/paa/US07_MERGED_COMB.pep1.*
31: /cgn2_6/ptodata/2/paa/US06_MERGED_COMB.pep1.*
32: /cgn2_6/ptodata/2/paa/PCT_MERGED_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	1	PCT-US95-03316-2 Sequence 2, Appli

2	760	100.0	148	1	PCT-US95-03537-2 Sequence 2, Appli
3	760	100.0	148	6	US-08-214-581-2 Sequence 2, Appli
4	760	100.0	148	6	US-08-214-582-2 Sequence 2, Appli
5	760	100.0	148	6	US-08-215-086-2 Sequence 2, Appli
6	760	100.0	148	6	US-08-215-087-2 Sequence 2, Appli
7	760	100.0	148	6	US-08-215-088-2 Sequence 2, Appli
8	760	100.0	148	6	US-08-227-369-2 Sequence 2, Appli
9	760	100.0	148	6	US-08-227-371-2 Sequence 2, Appli
10	760	100.0	148	18	US-09-480-135-16 Sequence 16, Appli
11	760	100.0	148	18	US-09-480-135-24 Sequence 24, Appli
12	760	100.0	148	28	US-09-016-869B-35 Sequence 35, Appli
13	760	100.0	156	6	US-08-248-812-2 Sequence 2, Appli
14	760	100.0	156	7	US-08-306-511-2 Sequence 2, Appli
15	760	100.0	156	8	US-08-497-214A-2 Sequence 2, Appli
16	760	100.0	156	8	US-08-497-214B-2 Sequence 2, Appli
17	760	100.0	156	8	US-08-497-214C-2 Sequence 2, Appli
18	760	100.0	156	8	US-08-497-214D-2 Sequence 2, Appli
19	760	100.0	156	9	US-08-581-918-2 Sequence 2, Appli
20	760	100.0	156	14	US-09-016-537A-2 Sequence 2, Appli
21	760	100.0	156	14	US-09-016-750-2 Sequence 2, Appli
22	760	100.0	156	14	US-09-016-750C-2 Sequence 2, Appli
23	760	100.0	156	14	US-09-016-869A-2 Sequence 2, Appli
24	760	100.0	156	23	US-09-947-206-2 Sequence 2, Appli
25	760	100.0	156	28	US-09-016-869B-2 Sequence 2, Appli
26	760	100.0	391	13	US-08-902-572-2 Sequence 2, Appli
27	760	100.0	391	18	US-09-457-568-4 Sequence 4, Appli
28	760	100.0	391	18	US-09-457-646-4 Sequence 4, Appli
29	760	100.0	391	19	US-09-516-065-4 Sequence 4, Appli
30	760	100.0	391	21	US-09-718-233-2 Sequence 2, Appli
31	753	99.1	148	6	US-08-251-938-2 Sequence 2, Appli
32	753	99.1	148	14	US-09-075-505-2 Sequence 2, Appli
33	753	99.1	156	8	US-08-474-083-2 Sequence 2, Appli
34	753	99.1	156	8	US-08-479-731-2 Sequence 2, Appli
35	753	99.1	156	8	US-08-481-063-2 Sequence 2, Appli
36	753	99.1	156	9	US-08-502-881-2 Sequence 2, Appli
37	753	99.1	156	14	US-09-021-752-2 Sequence 2, Appli
38	753	99.1	156	14	US-09-075-505-3 Sequence 3, Appli
39	753	99.1	156	16	US-09-272-233-2 Sequence 2, Appli
40	753	99.1	156	18	US-09-457-568-28 Sequence 28, Appli
41	753	99.1	156	18	US-09-457-646-28 Sequence 28, Appli
42	753	99.1	156	19	US-09-516-065-28 Sequence 28, Appli
43	753	99.1	156	20	US-09-614-099-19 Sequence 19, Appli
44	753	99.1	156	22	US-09-849-626-1908 Sequence 1908, Ap
45	753	99.1	156	26	US-10-017-754-1908 Sequence 1908, Ap

ALIGNMENTS

RESULT 1
PCT-US95-03316-2
; Sequence 2, Application PC/TUS9503316
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS
; TITLE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF
; TITLE OF INVENTION: CANCER DUE TO THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE:

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FILING DATE: 18-MAR-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-214-581-2

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
QY 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148

RESULT 4
US-08-214-582-2
Sequence 2, Application US/08214582
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,582
FILING DATE: 18-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-214-582-2

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
QY 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148

RESULT 5
US-08-215-086-2
Sequence 2, Application US/08215086
GENERAL INFORMATION:
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Skolnick, Mark H.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,086
FILING DATE: 18-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-215-086-2

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLHGA 60
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
QY 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGRGNSHARIDAEGPSDIPD 148


```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-369-2

Query Match          100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
   |||||
Db 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
   |||||

QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
   |||||
Db 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
   |||||

QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
   |||||
Db 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
   |||||

RESULT 9
US-08-227-371-2
; Sequence 2, Application US/08227371
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Protein, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,371
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-869b-35.rapm

Query Match          100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
   |||||
Db 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
   |||||

QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
   |||||
Db 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
   |||||

QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
   |||||
Db 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
   |||||

RESULT 10
US-09-480-135-16
; Sequence 16, Application US/09480135
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC
; STREET: 1100 New York Ave., Suite 600, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,135
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/384,106
; FILING DATE: 06-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-480-135-16

Query Match          100.0%; Score 760; DB 18; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
```

Db 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQQVMMGSAARVAELLHLHGA 60
QY 61 EPNCADPATLTPRVHDAAREGFDTLVVHLHRAGARLDVRDAGRLPVDLAELGLHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFDTLVVHLHRAGARLDVRDAGRLPVDLAELGLHRDVAR 120
QY 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
Db 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
RESULT 11
US-09-480-135-24
; Sequence 24, Application US/09480135
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hiral Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: InK4c-p18 and InK4c-p19, Inhibitors of
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC
; STREET: 1100 New York Ave., Suite 600, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,135
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/384,106
; FILING DATE: 06-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-480-135-24
Query Match 100.0%; Score 760; DB 18; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQQVMMGSAARVAELLHLHGA 60
QY 61 EPNCADPATLTPRVHDAAREGFDTLVVHLHRAGARLDVRDAGRLPVDLAELGLHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFDTLVVHLHRAGARLDVRDAGRLPVDLAELGLHRDVAR 120
QY 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148

Db 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
RESULT 12
US-09-016-869B-35
; Sequence 35, Application US/09016869B
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
; TITLE OF INVENTION: Uses Related Thereto
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ropes & Gray
; STREET: One International Place
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,869B
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/893,274
; FILING DATE: 15-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: GPCI-P10-071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 951-7739
; TELEFAX: (617) 951-7050
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-869B-35
Query Match 100.0%; Score 760; DB 28; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQQVMMGSAARVAELLHLHGA 60
QY 61 EPNCADPATLTPRVHDAAREGFDTLVVHLHRAGARLDVRDAGRLPVDLAELGLHRDVAR 120

Db 61 EPCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Qy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148
|||||
Db 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148
RESULT 13
US-08-248-812-2
; Sequence 2, Application US/08248812
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; APPLICANT: Queller, Dawn E.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,812
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-812-2
Query Match 100.0%; Score 760; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPVQVMMGMSARVAELLLHGA 60
|||||
Db 9 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPVQVMMGMSARVAELLLHGA 68
Qy 61 EPCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
|||||
Db 69 EPCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128
Qy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148
|||||
Db 129 YLRAAGTGRGSHARIDAAEGPSDIPD 156
RESULT 14
US-08-306-511-2
; Sequence 2, Application US/08306511
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory
; TITLE OF INVENTION: Cell-cycle Regulatory Proteins and
; TITLE OF INVENTION: Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA

; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-306-511-2
Query Match 100.0%; Score 760; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPVQVMMGMSARVAELLLHGA 60
|||||
Db 9 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPVQVMMGMSARVAELLLHGA 68
Qy 61 EPCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
|||||
Db 69 EPCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128
Qy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148
|||||
Db 129 YLRAAGTGRGSHARIDAAEGPSDIPD 156
RESULT 15
US-08-497-214A-2
; Sequence 2, Application US/08497214A
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory
; TITLE OF INVENTION: Cell-cycle Regulatory Proteins and
; TITLE OF INVENTION: Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214A
FILING DATE: 30-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV071.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-497-214A-2

Query Match 100.0%; Score 760; DB 8; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRPQVMMMGSAEVLHGA 60
DB 9 MEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRPQVMMMGSAEVLHGA 68
QY 61 EPCADPATLTRPVHDAAREGEFDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120
DB 69 EPCADPATLTRPVHDAAREGEFDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 128
QY 121 YLRAAAGGTGSGNHARIDAAEGPSDIPD 148
DB 129 YLRAAAGGTGSGNHARIDAAEGPSDIPD 156

Search completed: May 7, 2002, 12:35:37
Job time: 207 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:40 ; Search time 8.7 Seconds
(without alignments)
239.553 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760
Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64870 seqs, 14081815 residues

Total number of hits satisfying chosen parameters: 64870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US05_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	99.1	156	1	PCT-US02-07826-41
2	753	99.1	156	5	US-09-947-206D-2
3	753	99.1	156	5	US-09-947-206C-2
4	753	99.1	156	6	US-10-097-340-41
5	753	99.1	156	6	US-10-113-872-1908
6	627.5	82.6	157	5	US-09-947-206D-12
7	627.5	82.6	157	5	US-09-947-206C-12
8	493.5	64.9	137	5	US-09-947-206D-4
9	493.5	64.9	137	5	US-09-947-206C-4
10	382	50.3	138	5	US-09-947-206D-13
11	382	50.3	138	5	US-09-947-206C-13
12	356	46.8	77	5	US-09-947-206D-8
13	356	46.8	77	5	US-09-947-206C-8
14	330	43.4	125	5	US-09-947-206D-6
15	330	43.4	125	5	US-09-947-206C-6
16	299.5	39.4	85	5	US-09-947-206D-11
17	299.5	39.4	85	5	US-09-947-206C-11
18	299.5	39.4	127	5	US-09-947-206D-14
19	299.5	39.4	127	5	US-09-947-206C-14
20	288.5	30.1	1360	1	US-10-113-872-1907
21	149.5	19.7	1360	1	PCT-US02-09288-12
22	146	19.2	1166	5	US-09-972-115A-6
23	137	18.0	1327	5	US-09-972-115A-8
24	136	17.9	399	1	PCT-US02-09288-23
25	131	17.2	844	5	US-09-573-655B-1268
26	129	17.0	1536	1	PCT-US02-09944-470

27	126	16.6	1333	5	US-09-972-115A-2	Sequence 2, Appli
28	124.5	16.4	349	1	PCT-US02-09944-451	Sequence 451, App
29	124.5	16.4	608	1	PCT-US02-09944-708	Sequence 708, App
30	122	16.1	182	1	PCT-US02-09944-429	Sequence 429, App
31	121	15.9	877	5	US-09-573-655B-941	Sequence 941, App
32	113.5	14.9	1715	6	US-10-117-229-6	Sequence 6, Appli
33	112.5	14.8	1715	1	PCT-US02-09288-26	Sequence 26, Appli
34	112.5	14.8	1715	6	US-10-117-229-2	Sequence 2, Appli
35	112	14.7	556	1	PCT-US02-09944-427	Sequence 427, App
36	111.5	14.7	1267	5	US-09-972-115A-4	Sequence 4, Appli
37	110	14.5	1270	1	PCT-US02-09944-696	Sequence 696, App
38	110	14.5	2067	1	PCT-US02-09944-778	Sequence 778, App
39	109.5	14.4	305	7	US-60-365-384-514	Sequence 514, App
40	109.5	14.4	305	7	US-60-365-384-515	Sequence 515, App
41	109.5	14.4	784	7	US-60-371-507-2	Sequence 2, Appli
42	109.5	14.4	1060	1	PCT-US02-09944-452	Sequence 452, App
43	108	14.2	654	6	US-10-002-945-123	Sequence 123, Appli
44	108	14.2	1762	6	US-10-117-229-7	Sequence 7, Appli
45	107	14.1	669	6	US-10-002-945-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1
PCT-US02-07826-41
; Sequence 41, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: Assessment, Prevention, and Therapy of Ovarian Cancer
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; CURRENT FILING DATE: 2002-03-14
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/276.025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325.149
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/276.026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324.967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311.732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325.102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323.580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-07826-41

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.le-69;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPPVQMMGSAVLAELLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPPVQMMGSAVLAELLLHGA 68
Qy 61 EPNCAADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAMGRUPVDIAEELGHRDVAR 120
Db 69 EPNCAADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAMGRUPVDIAEELGHRDVAR 128
Qy 121 YLRAAAGTGRGSHHARIDAEGPSDIPD 148
Db 129 YLRAAAGTGRGSHHARIDAEGPSDIPD 156

```
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-206C-2

Query Match          99.1%; Score 753; DB 5; Length 156;
Best Local Similarity 99.3%; Pred No. 1,le-69;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFSDWLATAAAARGVEEVYRALLEAVALPNAPNSYGRPRPIQVMMMGSRVAELLLLHGA 60
   |||||
Db 9 MEFSDWLATAAAARGVEEVYRALLEAVALPNAPNSYGRPRPIQVMMMGSRVAELLLLHGA 68
   |||||

QY 61 EPNCADPATITRVPHDAAREGFDLTLLVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120
   |||||
Db 69 EPNCADPATITRVPHDAAREGFDLTLLVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128
   |||||

QY 121 YLRAAAGTGRGSNHARIDAAEGPSDIPD 148
   |||||
Db 129 YLRAAAGTGRGSNHARIDAAEGPSDIPD 156
   |||||

RESULT 4
US-10-097-340-41
; Sequence 41, Application US/10097340
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAWATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ani SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; TITLE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-41

Query Match          99.1%; Score 753; DB 6; Length 156;
```

```
Best Local Similarity 99.3%; Pred. No. 1.1e-69;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQIVMMGSRVAELLLHGA 60
    |||||
Db 9 MEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRRPQIVMMGSRVAELLLHGA 68
    |||||
QY 61 EPNCADPATLRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
    |||||
Db 69 EPNCADPATLRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 128
    |||||

QY 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
    |||||
Db 129 YLRAAGGTRGSNHARIDAAEGSPDIPD 156
    |||||

RESULT 5
US-10-113-872-1908
; Sequence 1908, Application US/10113872
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1908
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-1908

Query Match 99.1%; Score 753; DB 6; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-69;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQIVMMGSRVAELLLHGA 60
    |||||
Db 9 MEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRRPQIVMMGSRVAELLLHGA 68
    |||||
QY 61 EPNCADPATLRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
    |||||
Db 69 EPNCADPATLRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 128
    |||||

QY 121 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
    |||||
Db 129 YLRAAGGTRGSNHARIDAAEGSPDIPD 156
    |||||

RESULT 6
US-09-947-2060-12
; Sequence 12, Application US/09947206D
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; APPLICANT: Hannon, G.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPCI-P14-071
; CURRENT APPLICATION NUMBER: US/09/947,206D
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; PRIOR APPLICATION NUMBER: 07/963,308
; PRIOR FILING DATE: 1992-10-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternate general formula representing amino acid sequence of
; OTHER INFORMATION: CCR-protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(157)

US-09-947-2060-12

Query Match 82.6%; Score 627.5; DB 5; Length 157;
Best Local Similarity 83.9%; Pred. No. 5.5e-57;
Matches 125; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQIVMMGSRVAELLLHGA 60
    |||||
Db 9 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQIVMMGSRVAELLLHGA 68
    |||||
QY 61 EPNCADPAT-LTRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVA 119
    |||||
Db 69 XXNCXDPXTXXRPPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVA 128
    |||||

QY 120 YLRAAGGTRGSNHARIDAAEGSPDIPD 148
    |||||
Db 129 YLRAAGGTRGSNHARIDAAEGSPDIPD 157
    |||||

RESULT 7
US-09-947-206C-12
; Sequence 12, Application US/09947206C
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; APPLICANT: Hannon, G.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPCI-P14-071
; CURRENT APPLICATION NUMBER: US/09/947,206C
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; PRIOR APPLICATION NUMBER: 07/963,308
; PRIOR FILING DATE: 1992-10-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternate general formula representing amino acid sequence of
; OTHER INFORMATION: CCR-protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(157)
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:30:35 ; Search time 12.51 seconds
(without alignments)
266.226 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760

Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHRIDAEGPSDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2.6/ptodata/2/iaa/PCU5_COMB.pep.*

6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	760	100.0	148	1 US-08-154-915-4	Sequence 4, Appli
2	760	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl
3	760	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl
4	760	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appli
5	760	100.0	156	2 US-08-627-610-2	Sequence 2, Appli
6	760	100.0	156	2 US-08-306-511A-2	Sequence 2, Appli
7	760	100.0	156	2 US-08-893-274-2	Sequence 2, Appli
8	760	100.0	156	3 US-08-581-918A-2	Sequence 2, Appli
9	760	100.0	156	4 US-08-346-147B-2	Sequence 2, Appli
10	760	100.0	156	4 US-08-822-936-2	Sequence 2, Appli
11	760	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appli
12	760	100.0	391	1 US-08-589-981-2	Sequence 2, Appli
13	753	99.1	156	1 US-08-474-177-2	Sequence 2, Appli
14	753	99.1	156	1 US-08-487-033-2	Sequence 2, Appli
15	753	99.1	156	1 US-08-480-810-2	Sequence 2, Appli
16	753	99.1	156	2 US-08-508-735-2	Sequence 2, Appli
17	753	99.1	156	2 US-08-848-251-2	Sequence 2, Appli
18	753	99.1	156	2 US-08-486-047-2	Sequence 2, Appli
19	753	99.1	156	3 US-09-120-130-2	Sequence 2, Appli
20	753	99.1	156	3 US-09-115-252-2	Sequence 2, Appli
21	753	99.1	156	3 US-08-986-515-2	Sequence 2, Appli
22	753	99.1	156	4 US-09-120-128-2	Sequence 2, Appli
23	753	99.1	156	4 US-09-120-129-2	Sequence 2, Appli
24	753	99.1	156	4 US-09-201-139-2	Sequence 2, Appli
25	753	99.1	156	4 US-09-120-131-2	Sequence 2, Appli
26	753	99.1	156	4 US-08-910-722-2	Sequence 2, Appli
27	749.5	98.6	157	5 PCT-US96-05252-5	Sequence 5, Appli

28 627.5 82.6 157 3 US-08-581-918A-12 Sequence 12, Appli

29 627.5 82.6 157 4 US-08-346-147B-12 Sequence 12, Appli

30 544 71.6 105 1 US-08-474-177-14 Sequence 14, Appli

31 544 71.6 105 1 US-08-487-033-14 Sequence 14, Appli

32 544 71.6 105 1 US-08-480-810-14 Sequence 14, Appli

33 544 71.6 105 2 US-08-508-735-14 Sequence 14, Appli

34 544 71.6 105 2 US-08-848-251-14 Sequence 14, Appli

35 544 71.6 105 3 US-08-486-047-14 Sequence 14, Appli

36 544 71.6 105 3 US-09-120-130-14 Sequence 14, Appli

37 544 71.6 105 3 US-09-115-252-14 Sequence 14, Appli

38 544 71.6 105 3 US-08-986-515-14 Sequence 14, Appli

39 544 71.6 105 4 US-09-120-128-14 Sequence 14, Appli

40 544 71.6 105 4 US-09-120-129-14 Sequence 14, Appli

41 544 71.6 105 4 US-09-201-139-14 Sequence 14, Appli

42 544 71.6 105 4 US-09-120-131-14 Sequence 14, Appli

43 533 70.1 130 2 US-08-627-610-8 Sequence 8, Appli

44 533 70.1 130 3 US-08-581-918A-8 Sequence 8, Appli

45 533 70.1 130 4 US-08-346-147B-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-08-154-915-4

; Sequence 4, Application US/08154915

; Patent No. 5618669

; GENERAL INFORMATION:

; APPLICANT: Beach, David

; APPLICANT: Xiong, Yue

; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses

; TITLE OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/154,915

; FILING DATE: 19-NOV-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/991,997

; FILING DATE: 17-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/963,308

; FILING DATE: 16-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/888,178

; FILING DATE: 26-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/701,514

; FILING DATE: 16-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MII-026

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 148 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
US-08-154-915-4

Query Match      100.0%; Score 760; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60

QY 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120

QY 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148
Db 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148

RESULT 3
US-08-384-106A-24
; Sequence 24, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: InK4c-p18 and InK4d-p19, Inhibitors of
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-384-106A-24

Query Match      100.0%; Score 760; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60

QY 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120

QY 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148
Db 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148

RESULT 4
```

```

; MOLECULE TYPE: protein
US-08-154-915-4

Query Match      100.0%; Score 760; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60

QY 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120

QY 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148
Db 121 YLRAAAGGTGRGSHARIDAAEGPSDIPD 148

RESULT 2
US-08-384-106A-16
; Sequence 16, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: InK4c-p18 and InK4d-p19, Inhibitors of
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-384-106A-16

Query Match      100.0%; Score 760; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLNPAPNSYGRRPVQVMMGSAARVAELLHLHGA 60
```

```
PCT-US93-09945-4
; Sequence 4, Application PC/TUS9309945
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09945
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-09945-4

Query Match 100.0%; Score 760; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 60
Db 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 60
QY 61 EPCNADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 EPCNADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
Db 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148

RESULT 5
US-08-627-610-2
; Sequence 2, Application US/08627610
; Patent No. 591997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
```

```
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-627-610-2

Query Match 100.0%; Score 760; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 68
QY 61 EPCNADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 69 EPCNADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 128
QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
Db 129 YLRAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 6
US-08-306-511A-2
; Sequence 2, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```


;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-581-918A-2

Query Match 100.0%; Score 760; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRRALLEAVLPNAPNSYGRRPPIQVMMGMSARVAELLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRRALLEAVLPNAPNSYGRRPPIQVMMGMSARVAELLLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
Db 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
Db 129 YLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 9
US-08-346-147B-2
; Sequence 2, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Therto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,147B
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.04
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-346-147B-2

Query Match 100.0%; Score 760; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRRALLEAVLPNAPNSYGRRPPIQVMMGMSARVAELLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRRALLEAVLPNAPNSYGRRPPIQVMMGMSARVAELLLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
Db 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148
Db 129 YLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 10
US-08-822-936-2
; Sequence 2, Application US/08822936
; Patent No. 6242575
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti
; TITLE OF INVENTION: and Uses of Said Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,936
; FILING DATE: 21-FEBRUARY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.05
; TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-936-2

Query Match 100.0%; Score 760; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 68
QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 120
Db 69 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 128
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148
Db 129 YLRAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 11
PCT-US95-04636-2
; Sequence 2, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04636-2

Query Match 100.0%; Score 760; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 120
Db 69 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 128
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148
Db 129 YLRAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 12
US-08-589-981-2
; Sequence 2, Application US/08589981
; Patent No. 5672508
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,981
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-589-981-2

Query Match 100.0%; Score 760; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 60
Db 244 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAEALLLHGA 303
QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 120
Db 304 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDANGRLPVDLAELGHRDVAR 363
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148
Db 364 YLRAAGGTRGSNHARIDAAEGPSDIPD 391

RESULT 13
US-08-474-177-2
; Sequence 2, Application US/08474177
; Patent No. 5624819

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-177-2

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEPSADWLATAARGVEEVRALLEAVLPNAPNSYGRPRIOVMMGMSARVAELLHGA 60
DB 9 MEPSADWLATAARGVEEVRALLEAGALPNAPNSYGRPRIOVMMGMSARVAELLHGA 68
QY 61 EPNCADPATLTRPVHDAAREGEFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120
DB 69 EPNCADPATLTRPVHDAAREGEFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148
DB 129 YLRAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 14
US-08-487-033-2
Sequence 2, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-033-2

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEPSADWLATAARGVEEVRALLEAVLPNAPNSYGRPRIOVMMGMSARVAELLHGA 60
DB 9 MEPSADWLATAARGVEEVRALLEAGALPNAPNSYGRPRIOVMMGMSARVAELLHGA 68
QY 61 EPNCADPATLTRPVHDAAREGEFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120
DB 69 EPNCADPATLTRPVHDAAREGEFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148
DB 129 YLRAAGGTRGSNHARIDAAEGPSDIPD 156

```

Db          |||||
129 YLRAAGGTRGSNHARIDAAEGSPDIP 156

Search completed: May 7, 2002, 12:33:23
Job time: 168 sec

```

	Query Match	99.1%	Score 753;	DB 1;	Length 156;
	Best Local Similarity	99.3%;	Pred. No. 1.1e-82;		
	Matches 147;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps
QY	1	MEPSADWLATAAARGRVEEVRALLEVALPNAPNSYGRRPITQVMMGARSARVAELLHGA	60		
Db	9	MEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPITQVMMGARSARVAELLHGA	68		
QY	61	EPNCADPATLTRPVHDAAREGGDLTVLVLHHRAGRLVDYDAGWGLPVDLAAEELGHRDVAR	120		
Db	69	EPNCADPATLTRPVHDAAREGFDLTVLVHHRAGRLVDYDAGWGLPVDLAAEELGHRDVAR	128		
QY	121	VYRAAAGTGTSNHARIDAAEGPSDIPD	148		